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# SEQUENCE LISTING

<110> Edinger, Shlomit R  
Gerlach, Valerie  
MacDougall, John R  
Malyankar, Muriel M  
Smithson, Glennda  
Millet, Isabelle  
Peyman, John A  
Stone, David J  
Gunther, Erik  
Ellerman, Karen  
Shimkets, Richard A  
Padigaru, Muralidhara  
Guo, Xiaojia  
Patturajan, Meera  
Taupier Jr, Raymond J  
Burgess, Catherine E  
Zerhusen, Bryan D  
Kekuda, Ramesh  
Spytek, Kimberly A  
Gangolli, Esha A  
Fernandes, Elma R  
Gorman, Linda

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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Cys	Leu	Arg	His	Lys	Arg	Ser	Leu	Leu	Arg	Ser	His	Arg	Asn	Glu	Glu	355	360	365
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Val	Ser	Ala	Leu	Phe	Lys	Asp	Gly	Leu	Met	Gly	Lys	Asp	Gly	Thr	Arg	405	410	415
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Asn	Glu	Pro	Cys	Asp	Thr	Leu	Gly	Phe	Ala	Pro	Ile	Ser	Gly	Met	Cys	435	440	445
Ser	Lys	Tyr	Arg	Ser	Cys	Thr	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Gly	Leu	450	455	460
Ala	Phe	Thr	Ile	Ala	His	Glu	Ser	Gly	His	Asn	Phe	Gly	Met	Ile	His	465	470	475
Asp	Gly	Glu	Gly	Asn	Met	Cys	Lys	Lys	Ser	Glu	Gly	Asn	Ile	Met	Ser	485	490	495
Pro	Thr	Leu	Ala	Gly	Arg	Asn	Gly	Val	Phe	Ser	Trp	Ser	Pro	Cys	Ser	500	505	510
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Glu	Lys	Ala	Lys	Leu	Cys	Met	Leu	Asp	Phe	Lys	Lys	Asp	Ile	Cys	Lys	565	570	575
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His 785	Arg	Gly	Leu	Tyr	Thr 790	Lys	His	His	His	Thr 795	Asn	Gln	Tyr	Tyr	His 800
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Ser 850	Gly	Thr	Thr	Phe	Asp	Tyr 855	Arg	Arg	Ser	Tyr	Asn 860	Glu	Pro	Glu	Asn
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Ile	Val 915	Arg	Ser	Glu	Cys	Ser	Val 920	Ser	Cys	Gly	Gly	Gly 925	Arg	Cys	Leu

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Phe Pro Ser Val Gln Lys Val Cys Leu Asp Leu Ser Pro Gly Tyr Ser
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Asp Val Lys Phe Thr Val Thr Leu Glu Thr Lys Asp Lys Thr Gln Lys
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Leu Leu Glu Tyr Ser Gly Leu Lys Lys Arg His Leu His Cys Ile Ser
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Phe Leu Val Pro Pro Pro Ala Gly Gly Thr Glu Glu Val Ala Thr Ile
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Pro	Leu	Tyr	Thr	Pro	Gly	Gln	Gln	Val	Tyr	Phe	Arg	Ile	Val	Thr	Met	130	135	140	
Asp	Ser	Asn	Phe	Val	Pro	Val	Asn	Asp	Lys	Tyr	Ser	Met	Val	Glu	Leu	145	150	155	160
Gln	Asp	Pro	Asn	Ser	Asn	Arg	Ile	Ala	Gln	Trp	Leu	Glu	Val	Val	Pro	165	170	175	
Glu	Gln	Gly	Ile	Val	Asp	Leu	Ser	Phe	Gln	Leu	Ala	Pro	Glu	Ala	Met	180	185	190	
Leu	Gly	Thr	Tyr	Thr	Val	Ala	Val	Ala	Glu	Gly	Lys	Thr	Phe	Gly	Thr	195	200	205	
Phe	Ser	Val	Glu	Glu	Tyr	Val	Leu	Ser	Pro	Phe	Leu	Leu	Leu	Leu	Ser	210	215	220	
Ser	Val	Leu	Pro	Lys	Phe	Lys	Val	Glu	Val	Val	Glu	Pro	Lys	Glu	Leu	225	230	235	240
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Ala	Asn	Thr	Tyr	Trp	Tyr	Arg	Glu	Val	Glu	Arg	Glu	Gln	Leu	Pro	Asp	275	280	285	
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 Gly Ser Arg Ser Ser Ser Asn Met Ala Ile Val Glu Val Lys Met Leu  
 1365 1370 1375  
 Ser Gly Phe Ser Pro Met Glu Gly Thr Asn Gln Leu Leu Leu Gln Gln  
 1380 1385 1390  
 Pro Leu Val Lys Lys Val Glu Phe Gly Thr Asp Thr Leu Asn Ile Tyr  
 1395 1400 1405  
 Leu Asp Glu Leu Ile Lys Asn Thr Gln Thr Tyr Thr Phe Thr Ile Ser  
 1410 1415 1420  
 Gln Ser Val Leu Val Thr Asn Leu Lys Pro Ala Thr Ile Lys Val Tyr  
 1425 1430 1435 1440  
 Asp Tyr Tyr Leu Pro Gly Ser Phe Lys Leu Ser Gln Tyr Thr Ile Val  
 1445 1450 1455  
 Trp Ser Met Asn Asn Asp Ser Ile Val Asp Ser Val Ala Arg His Pro  
 1460 1465 1470  
 Glu Pro Pro Pro Phe Lys Thr Glu Ala Phe Ile Pro Ser Leu Pro Gly  
 1475 1480 1485  
 Ser Val Asn Asn  
 1490

<210> 11  
 <211> 987  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
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 atgatggggc tgctcatgtt ctctttggga tgttccgtgg agatccggaa gctgtgggtcg 180  
 cacatcagga gacctgggg cattgctgtg ggactgctct gccagtttgg gctcatgcct 240  
 ttacagctt atctcctggc cattagcttt tctctgaagc cagtccaagc tattgctgtt 300  
 ctcatcatgg gctgctgccg gggggcacca tctctaacat ttccaccttc tgggttgatg 360  
 gagatatgga tctcaggtgc cctgggaatg atgccactct gcatttatct ctacacctgg 420  
 tcctggagtc ttcagcagaa tctcaccatt ccttatcaga acataggtct gtcttttagga 480  
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 ccaaaacaat ccaaaatcat tctcaaggcc gttgttggtg gggtcctcct tctgggtggtc 600  
 gcagttgctg gtgtgggtcct ggcgaaagga tcttgggaatt cagacatcac ccttctgacc 660  
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 caccagtctt ggcaaaggac cttgcctatc tttttaggtt tagctttcaa gacaccctgt 780  
 gataccctac tcgcaatgac ttcgtgtcct gaatgttcca ggctcatcta tgccttcatt 840

cctctgctat atggactctt ccagctgata gatggatttc ttattgttga agagagaaca 900  
gaagatacag actgcgatgg ttcaccttta cctgagtatt ttactgaggt aacaataata 960  
cctaaacaac ctaggatatg acagctt 987

<210> 12  
<211> 326  
<212> PRT  
<213> Homo sapiens

<400> 12  
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35 40 45  
Leu Gly Cys Ser Val Glu Ile Arg Lys Leu Trp Ser His Ile Arg Arg  
50 55 60  
Pro Trp Gly Ile Ala Val Gly Leu Leu Cys Gln Phe Gly Leu Met Pro  
65 70 75 80  
Phe Thr Ala Tyr Leu Leu Ala Ile Ser Phe Ser Leu Lys Pro Val Gln  
85 90 95  
Ala Ile Ala Val Leu Ile Met Gly Cys Cys Arg Gly Ala Pro Ser Leu  
100 105 110  
Thr Phe Ser Pro Ser Gly Leu Met Glu Ile Trp Ile Ser Gly Ala Leu  
115 120 125  
Gly Met Met Pro Leu Cys Ile Tyr Leu Tyr Thr Trp Ser Trp Ser Leu  
130 135 140  
Gln Gln Asn Leu Thr Ile Pro Tyr Gln Asn Ile Gly Leu Ser Leu Gly  
145 150 155 160  
Ile Thr Leu Val Cys Leu Thr Ile Pro Val Ala Phe Gly Val Tyr Val  
165 170 175  
Asn Tyr Arg Trp Pro Lys Gln Ser Lys Ile Ile Leu Lys Ala Val Val  
180 185 190  
Gly Gly Val Leu Leu Leu Val Val Ala Val Ala Gly Val Val Leu Ala  
195 200 205  
Lys Gly Ser Trp Asn Ser Asp Ile Thr Leu Leu Thr Ile Ser Phe Ile  
210 215 220  
Phe Pro Leu Ile Gly His Val Thr Gly Phe Leu Leu Ala Leu Phe Thr  
225 230 235 240  
His Gln Ser Trp Gln Arg Thr Leu Pro Ile Phe Leu Gly Leu Ala Phe

245	250	255
Lys Thr Pro Cys Asp Thr Leu Leu Ala Met Thr Ser Cys Pro Glu Cys		
260	265	270
Ser Arg Leu Ile Tyr Ala Phe Ile Pro Leu Leu Tyr Gly Leu Phe Gln		
275	280	285
Leu Ile Asp Gly Phe Leu Ile Val Glu Glu Arg Thr Glu Asp Thr Asp		
290	295	300
Cys Asp Gly Ser Pro Leu Pro Glu Tyr Phe Thr Glu Val Thr Ile Ile		
305	310	315
320		
Pro Lys Gln Pro Arg Ile		
325		

<210> 13  
 <211> 850  
 <212> DNA  
 <213> Homo sapiens

<400> 13

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catggttaca	gaaatcaata	atctttgact	gccgttctca	gccacgtaat	gtgccagtca	240
tcaccggtag	caaagattta	cagaatgtca	acctcacact	gcgcatcatc	ttccggcccc	300
tagctagcca	gcttcctcac	atcttcacca	gcagcggaga	ggaccatgat	gagcgtgtgc	360
cgccgtccat	cacgaacaag	atcctcaagt	cagtgggtggc	tcgctttgaa	gctggagaac	420
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tggtggaaaa	ggctgagcag	cagaaaaagg	cggccatcat	ttctgctgag	ggcgactcca	660
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cacctccgag						850

<210> 14  
 <211> 272  
 <212> PRT  
 <213> Homo sapiens

<400> 14

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		20					25						30		
Gly	His	Arg	Ala	Val	Val	Phe	Asp	Arg	Phe	Arg	Gly	Val	Gln	Asp	Ile
		35					40					45			
Val	Val	Gly	Lys	Gly	Thr	His	Cys	Leu	Ile	Pro	Trp	Leu	Gln	Lys	Ser

50	55	60
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Gly Ser Lys Asp Leu Gln Asn Val Asn Leu Thr Leu Arg Ile Ile Phe 85 90 95		
Arg Pro Val Ala Ser Gln Leu Pro His Ile Phe Thr Ser Ser Gly Glu 100 105 110		
Asp His Asp Glu Arg Val Pro Pro Ser Ile Thr Asn Lys Ile Leu Lys 115 120 125		
Ser Val Val Ala Arg Phe Glu Ala Gly Glu Leu Ile Thr Gln Arg Glu 130 135 140		
Gln Ile Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Pro Ala Ala Thr 145 150 155 160		
Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr Leu Thr Phe Gly 165 170 175		
Lys Glu Phe Ile Glu Ala Val Glu Ala Lys Gln Ile Ala Gln Gln Glu 180 185 190		
Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys 195 200 205		
Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Val Ala Glu Leu Ile 210 215 220		
Thr Asn Ser Leu Ala Thr Ala Gly Asp Ala Leu Ile Glu Leu Arg Lys 225 230 235 240		
Leu Glu Ala Val Glu Asp Ile Thr Tyr Gln Leu Leu Arg Ser Arg Asn 245 250 255		
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<210> 15  
 <211> 2011  
 <212> DNA  
 <213> Homo sapiens

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 gtgggtgcccg ggccttggca ggaggatgtg gcagatgctg aagagtgtgc tggtcgctgt 180  
 gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg ttgccaactg 240  
 ctgccatgga ctcaacactc gccccacacg aggctgcggc gttctgggcg ctgtgacctc 300  
 ttccagaaga aagactacgt acggacctgc atcatgaaca atgggggttgg gtaccggggc 360



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accatggcca cgaccgtggg tggcctgccc tgccaggctt ggagccacaa gttcccaaatt 420
gatcacaagt acacgcccac tctccggaat ggcctggaag agaacttctg ccgtaaccct 480
gatggcgacc ccggagggtcc ctggtgctac acaacagacc ctgctgtgcg cttccagagc 540
tgcggcacatca aatcctgccg ggaggccgcg tgtgtctggt gcaatggcga ggaataccgc 600
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caccagcacc ccttcgagcc gggcaagttc ctcgaccaag gtctggacga caactattgc 720
cggaatcctg acggctccga gcggccatgg tgctacacta cggatccgca gatcgagcga 780
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gcctgcttta cccacaactg ctgggtcctg gaaggaatta taatcccaaa ccgagtatgc 1920
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aaggatcatga gactgggtta ggcccagcct t 2011

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<210> 16  
 <211> 666  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
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 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr  
 20 25 30  
 Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu  
 35 40 45  
 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met  
 50 55 60  
 Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu  
 65 70 75 80  
 Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly  
 85 90 95  
 Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met  
 100 105 110

Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly			
		115					120					125						
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr			
	130					135					140							
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro			
145					150					155					160			
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val			
				165					170					175				
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val			
			180					185					190					
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser			
		195					200					205						
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro			
	210					215					220							
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys			
225					230					235					240			
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro			
				245					250					255				
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala			
			260					265					270					
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly			
		275					280					285						
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys			
	290					295					300							
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu			
305					310					315					320			
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp			
				325					330					335				
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala			
			340					345					350					
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln			
		355					360					365						
Thr	Ala	Thr	Thr	Ala	Gln	Gly	Ser	Ser	Thr	Ala	Ala	Arg	Ser	Ala	Arg			
	370					375					380							
Pro	Ala	Arg	Val	Ser	Ser	Ala	Ser	Ala	Gly	Pro	Leu	Arg	Arg	Arg	Thr			
385					390					395					400			
Ser	Arg	Ser	Ser	Arg	Leu	Pro	Pro	Asn	Arg	Met	His	Asn	Trp	Arg	Arg			
				405					410					415				

Thr Ser Ala Gly Thr Gln Met Gly Ile Ala Met Gly Pro Gly Ala Thr  
 420 425 430  
 Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val Pro Cys Asp Ala Ala  
 435 440 445  
 Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro Gln Thr Arg Cys Ser  
 450 455 460  
 Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp Ile Ser Gly Val Pro  
 465 470 475 480  
 Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln Ser  
 485 490 495  
 Ala Cys Gly Ile Gly Met Leu Pro Leu Thr Gly Tyr Glu Val Trp Leu  
 500 505 510  
 Gly Thr Leu Phe Gln Asn Pro Gln His Gly Glu Pro Ser Leu Gln Arg  
 515 520 525  
 Val Pro Val Ala Lys Met Val Cys Gly Pro Ser Gly Ser Gln Leu Val  
 530 535 540  
 Leu Leu Lys Leu Glu Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu  
 545 550 555 560  
 Ile Cys Leu Pro Pro Glu Trp Tyr Val Val Pro Pro Gly Thr Lys Cys  
 565 570 575  
 Glu Ile Ala Gly Trp Gly Glu Thr Lys Gly Thr Gly Asn Asp Thr Val  
 580 585 590  
 Leu Asn Val Ala Leu Leu Asn Val Ile Ser Asn Gln Glu Cys Asn Ile  
 595 600 605  
 Lys His Arg Gly Arg Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr  
 610 615 620  
 His Asn Cys Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys  
 625 630 635 640  
 Ala Arg Ser Cys Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val  
 645 650 655  
 Asp Trp Ile His Lys Val Met Arg Leu Gly  
 660 665

<210> 17  
 <211> 634  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
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tacatgaagg agggaggagt ggggaactgct ttgcgaaaaa tggacgcaat ggccaagcca 180  
gattgtatca tcacttgtga tggcaaaaac ctcaccataa aaaccgagag cactttgaaa 240  
acacagtttt cttgtaccct gggagagaag tttgaagaaa ccacagctga tggcagaaaa 300  
actcagactg tgtgcagctt tgcagatggt gcattgggtc agcatcagga gtgggatggg 360  
aaggaaaaca caataacaag aaaactgaaa gatgggaaat tagtggtgta ctgtgtcatg 420  
aacaatgtcg cctgtactcg gatctatgaa aaagtagaat aaaaattcca tcatcacttt 480  
ggacaggagt taactaatag aatgatcaag ctcagttcaa tgagcaaate tccatagtgt 540  
tttttttcat tactgtgttc aattatcttt atcacaaacg tttcacatgc agctatttca 600  
aagtgtcttg gattaattag gatcatccct ttgg 634

<210> 18  
<211> 134  
<212> PRT  
<213> Homo sapiens

<400> 18  
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Lys Arg Phe Asp Glu Tyr Met Lys Glu Gly Gly Val Gly Thr Ala Leu  
20 25 30  
Arg Lys Met Asp Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp  
35 40 45  
Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Gln Phe  
50 55 60  
Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly Arg  
65 70 75 80  
Lys Thr Gln Thr Val Cys Ser Phe Ala Asp Gly Ala Leu Val Gln His  
85 90 95  
Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Thr Arg Lys Leu Lys Asp  
100 105 110  
Gly Lys Leu Val Val Tyr Cys Val Met Asn Asn Val Ala Cys Thr Arg  
115 120 125  
Ile Tyr Glu Lys Val Glu  
130

<210> 19  
<211> 822  
<212> DNA  
<213> Homo sapiens

<400> 19  
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gagccgcatc tggctgtctg tgggtgttcat ctttcgtgtg ctgggtgtacg tgggtggcagc 120  
ggaggagggtg tgggacgatg agcagaagga ctttgtctgc aacaccaagc agcccggctg 180  
ccccaacgtc tgctatgacg agttcttccc cgtgtccccc gtgcgcctct gggccctaca 240  
gctcatcctg gtcacgtgcc cctcactgct cgtgggtcatg cacgtggcct accgcgagga 300  
acgcgagcgc aagcaccacc tgaaacacgg gcccaatgcc ccgtccctgt acgacaacct 360

gagcaagaag cggggcggac tgtggtggac gtacttgctg agcctcatct tcaaggccgc 420  
cgtggatgct ggcttcctct atatcttcca ccgcctctac aaggattatg acatgccccg 480  
cgtggtggcc tgctccgtgg agccttgccc ccacactgtg gactgttaca tctcccggcc 540  
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gcaccggcgg cctcgggtgcc gggaatgcct acccgatacg tgcccaccat atgtcctctc 720  
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<210> 20  
<211> 266  
<212> PRT  
<213> Homo sapiens

<400> 20

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20 25 30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln  
35 40 45

Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys  
50 55 60

Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn  
100 105 110

Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly  
130 135 140

Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg  
145 150 155 160

Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr  
165 170 175

Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr  
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu  
195 200 205

Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro  
210 215 220

Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser  
225 230 235 240

Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly  
245 250 255

Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro  
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<210> 21  
<211> 546  
<212> DNA  
<213> Homo sapiens

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tgtgaactaa atccacagcc acataataat caaaacagaa aagcaaaaaga aagccacttc 180  
aggaaatacc acggtcacac ctgagttggc ttcattgctac agattataga aaatatgttg 240  
ctgcccgggc caccaatctg ttggttcaca ttactacgtg agcaatgtaa gtgtttgcaa 300  
gaagccatcc actatctaaa tatcagatat agatgctcca aagcagctac gtcagtgatg 360  
agaacagaga aaatacgtag caacatttca ttaagttgaa ttctaatact taaaaggctc 420  
cttttagtac tgacattctg gatTTTTAAAA gttatgttga ccgcatgttc tcactcacia 480  
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tgtcag 546

<210> 22  
<211> 61  
<212> PRT  
<213> Homo sapiens

<400> 22  
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20 25 30  
His Tyr Leu Asn Ile Arg Tyr Arg Cys Ser Lys Ala Ala Thr Ser Val  
35 40 45  
Met Arg Thr Glu Lys Ile Arg Ser Asn Ile Ser Leu Ser  
50 55 60

<210> 23  
<211> 2309  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> Wherein n is an a o t t o r c o r g.

<400> 23

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<210> 24

<211> 547

<212> PRT

<213> Homo sapiens

<400> 24

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                20                      25                      30

Lys Glu Arg Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn
  35                      40                      45

```

Leu	Val	Lys	Lys	Tyr	Cys	Pro	Lys	Arg	Ser	Ser	Lys	Asp	Glu	Glu	Pro
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Val	Tyr	Gly	Glu	Leu	Met	Arg	Tyr	Ala	His	Asp	Leu	Lys	Thr	Glu	Arg
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Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe	Pro	Phe	Glu	Asp	Tyr	Ser	Gln
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Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr	Pro	Val	Gly	Lys	Ala	Lys	Gly
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Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro	Lys	Gly	Pro	Ala	Leu	Glu	Asp
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Phe	Ser	His	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg
			340					345					350		



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 370 375 380  
 Asp Pro Gly Ser Leu Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile  
 385 390 395 400  
 Asp Arg Leu Arg Met Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu  
 405 410 415  
 Val Glu Gly Lys Thr Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp  
 420 425 430  
 Ile Asn His Leu Val Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr  
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 Thr Asp Asp Ala Asn Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly  
 450 455 460  
 His His Asn Glu Phe Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro  
 465 470 475 480  
 Ala Ile Gly His Cys Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu  
 485 490 495  
 Gly Thr Leu Ala Met Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu  
 500 505 510  
 Asp Lys Gly Asp Gly Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu  
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 Gly Tyr Val Pro Thr Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser  
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<210> 25  
 <211> 1787  
 <212> DNA  
 <213> Homo sapiens

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 tggggctgca gatctgctgg agccttgggc atctcagact cactcaccac aaggagtaa 540  
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<210> 26

<211> 1787

<212> DNA

<213> Homo sapiens

<400> 26

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<210> 27
<211> 472
<212> PRT
<213> Homo sapiens
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 Ala Val Arg Pro His Gln Gly Ala Leu Val Glu Arg Ile Ile Pro His  
 290 295 300  
 Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Arg  
 305 310 315 320  
 Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu  
 325 330 335  
 Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp Val Ser  
 340 345 350  
 Gly Trp Gly His Thr His Pro Ser His Thr Tyr Ser Ser Asp Met Leu  
 355 360 365  
 Gln Asp Thr Val Val Pro Leu Leu Ser Thr Gln Leu Cys Asn Ser Ser  
 370 375 380  
 Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala Gly Tyr  
 385 390 395 400  
 Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu  
 405 410 415  
 Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val Ser Trp  
 420 425 430  
 Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala Lys Val  
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<210> 28  
 <211> 2148  
 <212> DNA  
 <213> Homo sapiens

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<210> 29

<211> 418

<212> PRT

<213> Homo sapiens

<400> 29

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Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
          20             25             30

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Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
      35             40             45

```

```

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
      50             55             60

```

```

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
      65             70             75            80

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```

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
          85             90            95

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Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
      100            105            110

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Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly	
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Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys	
145					150					155					160	
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala	
				165					170					175		
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro	
			180					185					190			
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		195					200					205				
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	210					215					220					
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg	
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His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala	
				245					250					255		
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			260					265					270			
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		275					280					285				
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Gly	Tyr	Leu	Asp	Gly	Arg	Ala	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	
		355					360					365				
Pro	Leu	Val	Cys	Pro	Asp	Gly	Asp	Thr	Trp	Arg	Leu	Val	Gly	Val	Val	
	370					375					380					
Ser	Trp	Gly	Arg	Gly	Cys	Ala	Glu	Pro	Asn	His	Pro	Gly	Val	Tyr	Ala	
385					390					395					400	
Lys	Val	Ala	Glu	Phe	Leu	Asp	Trp	Ile	His	Asp	Thr	Ala	Gln	Asp	Ser	
				405					410					415		

Leu Leu

<210> 30

<211> 1593

<212> PRT

<213> Homo sapiens

<400> 30

Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala  
1 5 10 15

Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro  
20 25 30

Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly  
35 40 45

Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly  
50 55 60

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg  
65 70 75 80

Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser  
85 90 95

His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe  
100 105 110

Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His  
115 120 125

Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr  
130 135 140

Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys  
145 150 155 160

His Gly Leu Thr Gly Phe Phe Gln Leu Pro His Gly Asp Phe Phe Ile  
165 170 175

Glu Pro Val Lys Lys His Pro Leu Val Glu Gly Gly Tyr His Pro His  
180 185 190

Ile Val Tyr Arg Arg Gln Lys Val Pro Glu Thr Lys Glu Pro Thr Cys  
195 200 205

Gly Leu Lys Asp Ser Val Asn Ile Ser Gln Lys Gln Glu Leu Trp Arg  
210 215 220

Glu Lys Trp Glu Arg His Asn Leu Pro Ser Arg Ser Leu Ser Arg Arg  
225 230 235 240

Ser Ile Ser Lys Glu Arg Trp Val Glu Thr Leu Val Val Ala Asp Thr  
245 250 255

Lys	Met	Ile	Glu	Tyr	His	Gly	Ser	Glu	Asn	Val	Glu	Ser	Tyr	Ile	Leu	260	265	270
Thr	Ile	Met	Asn	Met	Val	Thr	Gly	Leu	Phe	His	Asn	Pro	Ser	Ile	Gly	275	280	285
Asn	Ala	Ile	His	Ile	Val	Val	Val	Arg	Leu	Ile	Leu	Leu	Glu	Glu	Glu	290	295	300
Glu	Gln	Gly	Leu	Lys	Ile	Val	His	His	Ala	Glu	Lys	Thr	Leu	Ser	Ser	305	310	315
Phe	Cys	Lys	Trp	Gln	Lys	Ser	Ile	Asn	Pro	Lys	Ser	Asp	Leu	Asn	Pro	325	330	335
Val	His	His	Asp	Val	Ala	Val	Leu	Leu	Thr	Arg	Lys	Asp	Ile	Cys	Ala	340	345	350
Gly	Phe	Asn	Arg	Pro	Cys	Glu	Thr	Leu	Gly	Leu	Ser	His	Leu	Ser	Gly	355	360	365
Met	Cys	Gln	Pro	His	Arg	Ser	Cys	Asn	Ile	Asn	Glu	Asp	Ser	Gly	Leu	370	375	380
Pro	Leu	Ala	Phe	Thr	Ile	Ala	His	Glu	Leu	Gly	His	Ser	Phe	Gly	Ile	385	390	395
Gln	His	Asp	Gly	Lys	Glu	Asn	Asp	Cys	Glu	Pro	Val	Gly	Arg	His	Pro	405	410	415
Tyr	Ile	Met	Ser	Arg	Gln	Leu	Gln	Tyr	Asp	Pro	Thr	Pro	Leu	Thr	Trp	420	425	430
Ser	Lys	Cys	Ser	Glu	Glu	Tyr	Ile	Thr	Arg	Phe	Leu	Asp	Arg	Gly	Trp	435	440	445
Gly	Phe	Cys	Leu	Asp	Asp	Ile	Pro	Lys	Lys	Lys	Gly	Leu	Lys	Ser	Lys	450	455	460
Val	Ile	Ala	Pro	Gly	Val	Ile	Tyr	Asp	Val	His	His	Gln	Cys	Gln	Leu	465	470	475
Gln	Tyr	Gly	Pro	Asn	Ala	Thr	Phe	Cys	Gln	Glu	Val	Glu	Asn	Val	Cys	485	490	495
Gln	Thr	Leu	Trp	Cys	Ser	Val	Lys	Gly	Phe	Cys	Arg	Ser	Lys	Leu	Asp	500	505	510
Ala	Ala	Ala	Asp	Gly	Thr	Gln	Cys	Gly	Glu	Lys	Lys	Trp	Cys	Met	Ala	515	520	525
Gly	Lys	Cys	Ile	Thr	Val	Gly	Lys	Lys	Pro	Glu	Ser	Ile	Pro	Gly	Gly	530	535	540
Trp	Gly	Arg	Trp	Ser	Pro	Trp	Ser	His	Cys	Ser	Arg	Thr	Cys	Gly	Ala	545	550	555



Gly	Val	Gln	Ser	Ala	Glu	Arg	Leu	Cys	Asn	Asn	Pro	Glu	Pro	Lys	Phe	565	570	575
Gly	Gly	Lys	Tyr	Cys	Thr	Gly	Glu	Arg	Lys	Arg	Tyr	Arg	Leu	Cys	Asn	580	585	590
Val	His	Pro	Cys	Arg	Ser	Glu	Ala	Pro	Thr	Phe	Arg	Gln	Met	Gln	Cys	595	600	605
Ser	Glu	Phe	Asp	Thr	Val	Pro	Tyr	Lys	Asn	Glu	Leu	Tyr	His	Trp	Phe	610	615	620
Pro	Ile	Phe	Asn	Pro	Ala	His	Pro	Cys	Glu	Leu	Tyr	Cys	Arg	Pro	Ile	625	630	635
Asp	Gly	Gln	Phe	Ser	Glu	Lys	Met	Leu	Asp	Ala	Val	Ile	Asp	Gly	Thr	645	650	655
Pro	Cys	Phe	Glu	Gly	Gly	Asn	Ser	Arg	Asn	Val	Cys	Ile	Asn	Gly	Ile	660	665	670
Cys	Lys	Met	Val	Gly	Cys	Asp	Tyr	Glu	Ile	Asp	Ser	Asn	Ala	Thr	Glu	675	680	685
Asp	Arg	Cys	Gly	Val	Cys	Leu	Gly	Asp	Gly	Ser	Ser	Cys	Gln	Thr	Val	690	695	700
Arg	Lys	Met	Phe	Lys	Gln	Lys	Glu	Gly	Ser	Gly	Tyr	Val	Asp	Ile	Gly	705	710	715
Leu	Ile	Pro	Lys	Gly	Ala	Arg	Asp	Ile	Arg	Val	Met	Glu	Ile	Glu	Gly	725	730	735
Ala	Gly	Asn	Phe	Leu	Ala	Ile	Arg	Ser	Glu	Asp	Pro	Glu	Lys	Tyr	Tyr	740	745	750
Leu	Asn	Gly	Gly	Phe	Ile	Ile	Gln	Trp	Asn	Gly	Asn	Tyr	Lys	Leu	Ala	755	760	765
Gly	Thr	Val	Phe	Gln	Tyr	Asp	Arg	Lys	Gly	Asp	Leu	Glu	Lys	Leu	Met	770	775	780
Ala	Thr	Gly	Pro	Thr	Asn	Glu	Ser	Val	Trp	Ile	Gln	Leu	Leu	Phe	Gln	785	790	795
Val	Thr	Asn	Pro	Gly	Ile	Lys	Tyr	Glu	Tyr	Thr	Ile	Gln	Lys	Asp	Gly	805	810	815
Leu	Asp	Asn	Asp	Val	Glu	Gln	Met	Tyr	Phe	Trp	Gln	Tyr	Gly	His	Trp	820	825	830
Thr	Glu	Cys	Ser	Val	Thr	Cys	Gly	Thr	Gly	Ile	Arg	Arg	Gln	Thr	Ala	835	840	845
His	Cys	Ile	Lys	Lys	Gly	Arg	Gly	Met	Val	Lys	Ala	Thr	Phe	Cys	Asp	850	855	860

Pro	Glu	Thr	Gln	Pro	Asn	Gly	Arg	Gln	Lys	Lys	Cys	His	Glu	Lys	Ala	865	870	875	880
Cys	Pro	Pro	Arg	Trp	Trp	Ala	Gly	Glu	Trp	Glu	Ala	Cys	Ser	Ala	Thr	885		890	895
Cys	Gly	Pro	His	Gly	Glu	Lys	Lys	Arg	Thr	Val	Leu	Cys	Ile	Gln	Thr	900		905	910
Met	Val	Ser	Asp	Glu	Gln	Ala	Leu	Pro	Pro	Thr	Asp	Cys	Gln	His	Leu	915		920	925
Leu	Lys	Pro	Lys	Thr	Leu	Leu	Ser	Cys	Asn	Arg	Asp	Ile	Leu	Cys	Pro	930		935	940
Ser	Asp	Trp	Thr	Val	Gly	Asn	Trp	Ser	Glu	Cys	Ser	Val	Ser	Cys	Gly	945		950	955
Gly	Gly	Val	Arg	Ile	Arg	Ser	Val	Thr	Cys	Ala	Lys	Asn	His	Asp	Glu	965		970	975
Pro	Cys	Asp	Val	Thr	Arg	Lys	Pro	Asn	Ser	Arg	Ala	Leu	Cys	Gly	Leu	980		985	990
Gln	Gln	Cys	Pro	Ser	Ser	Arg	Arg	Val	Leu	Lys	Pro	Asn	Lys	Gly	Thr	995		1000	1005
Ile	Ser	Asn	Gly	Lys	Asn	Pro	Pro	Thr	Leu	Lys	Pro	Val	Pro	Pro	Pro	1010		1015	1020
Thr	Ser	Arg	Pro	Arg	Met	Leu	Thr	Thr	Pro	Thr	Gly	Pro	Glu	Ser	Met	1025		1030	1035
Ser	Thr	Ser	Thr	Pro	Ala	Ile	Ser	Ser	Pro	Ser	Pro	Thr	Thr	Ala	Ser	1045		1050	1055
Lys	Glu	Gly	Asp	Leu	Gly	Gly	Lys	Gln	Trp	Gln	Asp	Ser	Ser	Thr	Gln	1060		1065	1070
Pro	Glu	Leu	Ser	Ser	Arg	Tyr	Leu	Ile	Ser	Thr	Gly	Ser	Thr	Ser	Gln	1075		1080	1085
Pro	Ile	Leu	Thr	Ser	Gln	Ser	Leu	Ser	Ile	Gln	Pro	Ser	Glu	Glu	Asn	1090		1095	1100
Val	Ser	Ser	Ser	Asp	Thr	Gly	Pro	Thr	Ser	Glu	Gly	Gly	Leu	Val	Ala	1105		1110	1115
Thr	Thr	Thr	Ser	Gly	Ser	Gly	Leu	Ser	Ser	Ser	Arg	Asn	Pro	Ile	Thr	1125		1130	1135
Trp	Pro	Val	Thr	Pro	Phe	Tyr	Asn	Thr	Leu	Thr	Lys	Gly	Pro	Glu	Met	1140		1145	1150
Glu	Ile	His	Ser	Gly	Ser	Gly	Glu	Glu	Arg	Glu	Gln	Pro	Glu	Asp	Lys	1155		1160	1165

Asp Glu Ser Asn Pro Val Ile Trp Thr Lys Ile Arg Val Pro Gly Asn  
 1170 1175 1180

Asp Ala Pro Val Glu Ser Thr Glu Met Pro Leu Ala Pro Pro Leu Thr  
 1185 1190 1195 1200

Pro Asp Leu Ser Arg Glu Ser Trp Trp Pro Pro Phe Ser Thr Val Met  
 1205 1210 1215

Glu Gly Leu Leu Pro Ser Gln Arg Pro Thr Thr Ser Glu Thr Gly Thr  
 1220 1225 1230

Pro Arg Val Glu Gly Met Val Thr Glu Lys Pro Ala Asn Thr Leu Leu  
 1235 1240 1245

Pro Leu Gly Gly Asp His Gln Pro Glu Pro Ser Gly Lys Thr Ala Asn  
 1250 1255 1260

Arg Asn His Leu Lys Leu Pro Asn Asn Met Asn Gln Thr Lys Ser Ser  
 1265 1270 1275 1280

Glu Pro Val Leu Thr Glu Glu Asp Ala Thr Ser Leu Ile Thr Glu Gly  
 1285 1290 1295

Phe Leu Leu Asn Ala Ser Asn Tyr Lys Gln Leu Thr Asn Gly His Gly  
 1300 1305 1310

Ser Ala His Trp Ile Val Gly Asn Trp Ser Glu Cys Ser Thr Thr Cys  
 1315 1320 1325

Gly Leu Gly Ala Tyr Trp Lys Arg Val Glu Cys Thr Thr Gln Met Asp  
 1330 1335 1340

Ser Asp Cys Ala Ala Ile Gln Arg Pro Asp Pro Ala Lys Arg Cys His  
 1345 1350 1355 1360

Leu Arg Pro Cys Ala Gly Trp Lys Val Gly Asn Trp Ser Lys Cys Ser  
 1365 1370 1375

Arg Asn Cys Ser Gly Gly Phe Lys Ile Arg Glu Ile Gln Cys Val Asp  
 1380 1385 1390

Ser Arg Asp His Arg Asn Leu Arg Pro Phe His Cys Gln Phe Leu Ala  
 1395 1400 1405

Gly Ile Pro Pro Pro Leu Ser Met Ser Cys Asn Pro Glu Pro Cys Glu  
 1410 1415 1420

Ala Trp Gln Val Glu Pro Trp Ser Gln Cys Ser Arg Ser Cys Gly Gly  
 1425 1430 1435 1440

Gly Val Gln Glu Arg Gly Val Phe Cys Pro Gly Gly Leu Cys Asp Trp  
 1445 1450 1455

Thr Lys Arg Pro Thr Ser Thr Met Ser Cys Asn Glu His Leu Cys Cys  
 1460 1465 1470

His Trp Ala Thr Gly Asn Trp Asp Leu Cys Ser Thr Ser Cys Gly Gly  
 1475 1480 1485  
 Gly Phe Gln Lys Arg Ile Val Gln Cys Val Pro Ser Glu Gly Asn Lys  
 1490 1495 1500  
 Thr Glu Asp Gln Asp Gln Cys Leu Cys Asp His Lys Pro Arg Pro Pro  
 1505 1510 1515 1520  
 Glu Phe Lys Lys Cys Asn Gln Gln Ala Cys Lys Lys Ser Ala Asp Leu  
 1525 1530 1535  
 Leu Cys Thr Lys Asp Lys Leu Ser Ala Ser Phe Cys Gln Thr Leu Lys  
 1540 1545 1550  
 Ala Met Lys Lys Cys Ser Val Pro Thr Val Arg Ala Glu Cys Cys Phe  
 1555 1560 1565  
 Ser Cys Pro Gln Thr His Ile Thr His Thr Gln Arg Gln Arg Arg Gln  
 1570 1575 1580  
 Arg Leu Leu Gln Lys Ser Lys Glu Leu  
 1585 1590

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<400> 31  
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 Phe Pro Thr Arg Val Asp His Asn Gly Ala Leu Leu Ala Phe Ser Pro  
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 Pro Pro Pro Arg Arg Gln Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser  
 35 40 45  
 Arg Leu Phe Tyr Lys Val Ala Ser Pro Ser Thr His Phe Leu Leu Asn  
 50 55 60  
 Leu Thr Arg Ser Ser Arg Leu Leu Ala Gly His Val Ser Val Glu Tyr  
 65 70 75 80  
 Trp Thr Arg Glu Gly Leu Ala Trp Gln Arg Ala Ala Arg Pro His Cys  
 85 90 95  
 Leu Tyr Ala Gly His Leu Gln Gly Gln Ala Ser Ser Ser His Val Ala  
 100 105 110  
 Ile Ser Thr Cys Gly Gly Leu His Gly Leu Ile Val Ala Asp Glu Glu  
 115 120 125  
 Glu Tyr Leu Ile Glu Pro Leu His Gly Gly Pro Lys Gly Ser Arg Ser

130					135					140					
Pro	Glu	Glu	Ser	Gly	Pro	His	Val	Val	Tyr	Lys	Arg	Ser	Ser	Leu	Arg
145					150					155					160
His	Pro	His	Leu	Asp	Thr	Ala	Cys	Gly	Val	Arg	Asp	Glu	Lys	Pro	Trp
				165					170					175	
Lys	Gly	Arg	Pro	Trp	Trp	Leu	Arg	Thr	Leu	Lys	Pro	Pro	Pro	Ala	Arg
			180					185					190		
Pro	Leu	Gly	Asn	Glu	Thr	Glu	Arg	Gly	Gln	Pro	Gly	Leu	Lys	Arg	Ser
		195					200					205			
Val	Ser	Arg	Glu	Arg	Tyr	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Lys	Met
	210					215					220				
Met	Val	Ala	Tyr	His	Gly	Arg	Arg	Asp	Val	Glu	Gln	Tyr	Val	Leu	Ala
225					230					235					240
Ile	Met	Asn	Ile	Val	Ala	Lys	Leu	Phe	Gln	Asp	Ser	Ser	Leu	Gly	Ser
				245					250					255	
Thr	Val	Asn	Ile	Leu	Val	Thr	Arg	Leu	Ile	Leu	Leu	Thr	Glu	Asp	Gln
			260					265					270		
Pro	Thr	Leu	Glu	Ile	Thr	His	His	Ala	Gly	Lys	Ser	Leu	Asp	Ser	Phe
		275					280					285			
Cys	Lys	Trp	Gln	Lys	Ser	Ile	Val	Asn	His	Ser	Gly	His	Gly	Asn	Ala
	290					295					300				
Ile	Pro	Glu	Asn	Gly	Val	Ala	Asn	His	Asp	Thr	Ala	Val	Leu	Ile	Thr
305					310					315					320
Arg	Tyr	Asp	Ile	Cys	Ile	Tyr	Lys	Asn	Lys	Pro	Cys	Gly	Thr	Leu	Gly
				325					330					335	
Leu	Ala	Pro	Val	Gly	Gly	Met	Cys	Glu	Arg	Glu	Arg	Ser	Cys	Ser	Val
			340					345					350		
Asn	Glu	Asp	Ile	Gly	Leu	Pro	Gln	Ala	Phe	Thr	Ile	Ala	His	Glu	Ile
		355					360					365			
Gly	His	Thr	Phe	Gly	Met	Asn	His	Asp	Gly	Val	Gly	Asn	Ser	Cys	Gly
	370					375					380				
Ala	Arg	Gly	Gln	Asp	Pro	Ala	Lys	Leu	Met	Ala	Ala	His	Ile	Thr	Met
385					390					395					400
Lys	Thr	Asn	Pro	Phe	Val	Trp	Ser	Ser	Cys	Asn	Arg	Asp	Tyr	Ile	Thr
				405					410					415	
Ser	Phe	Leu	Asp	Ser	Gly	Leu	Gly	Leu	Cys	Leu	Asn	Asn	Arg	Pro	Pro
			420					425					430		
Arg	Gln	Asp	Phe	Val	Tyr	Pro	Thr	Val	Ala	Pro	Gly	Gln	Ala	Tyr	Asp

435					440					445					
Ala	Asp	Glu	Gln	Cys	Arg	Phe	Gln	His	Gly	Val	Lys	Ser	Arg	Gln	Cys
450					455					460					
Lys	Tyr	Gly	Glu	Val	Cys	Ser	Glu	Leu	Trp	Cys	Leu	Ser	Lys	Ser	Asn
465					470					475					480
Arg	Cys	Ile	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	Gly	Thr	Leu	Cys	Gln
				485					490					495	
Thr	His	Thr	Ile	Asp	Lys	Gly	Trp	Cys	Tyr	Lys	Arg	Val	Cys	Val	Pro
			500					505					510		
Phe	Gly	Ser	Arg	Pro	Glu	Gly	Val	Asp	Gly	Ala	Trp	Gly	Pro	Trp	Thr
		515					520					525			
Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	Ser	Ser
		530					535					540			
Ser	Arg	His	Cys	Asp	Ser	Pro	Arg	Pro	Thr	Ile	Gly	Gly	Lys	Tyr	Cys
545					550					555					560
Leu	Gly	Glu	Arg	Arg	Arg	His	Arg	Ser	Cys	Asn	Thr	Asp	Asp	Cys	Pro
				565					570					575	
Pro	Gly	Ser	Gln	Asp	Phe	Arg	Glu	Val	Gln	Cys	Ser	Glu	Phe	Asp	Ser
			580					585					590		
Ile	Pro	Phe	Arg	Gly	Lys	Phe	Tyr	Lys	Trp	Lys	Thr	Tyr	Arg	Gly	Gly
		595					600					605			
Gly	Val	Lys	Ala	Cys	Ser	Leu	Thr	Ser	Leu	Ala	Glu	Gly	Phe	Asn	Phe
						615					620				
Tyr	Thr	Glu	Arg	Ala	Ala	Ala	Val	Val	Asp	Gly	Thr	Pro	Cys	Arg	Pro
625					630					635					640
Asp	Thr	Val	Asp	Ile	Cys	Val	Ser	Gly	Glu	Cys	Lys	His	Val	Gly	Cys
				645					650					655	
Asp	Arg	Val	Leu	Gly	Ser	Asp	Leu	Arg	Glu	Asp	Lys	Cys	Arg	Val	Cys
			660					665					670		
Gly	Gly	Asp	Gly	Ser	Ala	Cys	Glu	Thr	Ile	Glu	Gly	Val	Phe	Ser	Pro
		675					680					685			
Ala	Ser	Pro	Gly	Ala	Gly	Tyr	Glu	Asp	Val	Val	Trp	Ile	Pro	Lys	Gly
						695					700				
Ser	Val	His	Ile	Phe	Ile	Gln	Asp	Leu	Asn	Leu	Ser	Leu	Ser	His	Leu
705					710					715					720
Ala	Leu	Lys	Gly	Asp	Gln	Glu	Ser	Leu	Leu	Leu	Glu	Gly	Leu	Pro	Gly
				725					730					735	
Thr	Pro	Gln	Pro	His	Arg	Leu	Pro	Leu	Ala	Gly	Thr	Thr	Phe	Gln	Leu

740							745					750				
Arg	Gln	Gly	Pro	Asp	Gln	Val	Gln	Ser	Leu	Glu	Ala	Leu	Gly	Pro	Ile	
		755							760				765			
Asn	Ala	Ser	Leu	Ile	Val	Met	Val	Leu	Ala	Arg	Thr	Glu	Leu	Pro	Ala	
	770					775				780						
Leu	Arg	Tyr	Arg	Phe	Asn	Ala	Pro	Ile	Ala	Arg	Asp	Ser	Leu	Pro	Pro	
785					790					795					800	
Tyr	Ser	Trp	His	Tyr	Ala	Pro	Trp	Thr	Lys	Cys	Ser	Ala	Gln	Cys	Ala	
			805					810					815			
Gly	Gly	Ser	Gln	Val	Gln	Ala	Val	Glu	Cys	Arg	Asn	Gln	Leu	Asp	Ser	
			820					825					830			
Ser	Ala	Val	Ala	Pro	His	Tyr	Cys	Ser	Ala	His	Ser	Lys	Leu	Pro	Lys	
		835						840					845			
Arg	Gln	Arg	Ala	Cys	Asn	Thr	Glu	Pro	Cys	Pro	Pro	Asp	Trp	Val	Val	
						855							860			
Gly	Asn	Trp	Ser	Leu	Cys	Ser	Arg	Ser	Cys	Asp	Ala	Gly	Val	Arg	Ser	
865					870					875					880	
Arg	Ser	Val	Val	Cys	Gln	Arg	Arg	Val	Ser	Ala	Ala	Glu	Glu	Lys	Ala	
				885					890					895		
Leu	Asp	Asp	Ser	Ala	Cys	Pro	Gln	Pro	Arg	Pro	Pro	Val	Leu	Glu	Ala	
			900					905					910			
Cys	His	Gly	Pro	Thr	Cys	Pro	Pro	Glu	Trp	Ala	Ala	Leu	Asp	Trp	Ser	
		915						920					925			
Glu	Cys	Thr	Pro	Ser	Cys	Gly	Pro	Gly	Leu	Arg	His	Arg	Val	Val	Leu	
		930				935					940					
Cys	Lys	Ser	Ala	Asp	His	Arg	Ala	Thr	Leu	Pro	Pro	Ala	His	Cys	Ser	
945					950					955					960	
Pro	Ala	Ala	Lys	Pro	Pro	Ala	Thr	Met	Arg	Cys	Asn	Leu	Arg	Arg	Cys	
				965					970					975		
Pro	Pro	Ala	Arg	Trp	Val	Ala	Gly	Glu	Trp	Gly	Glu	Cys	Ser	Ala	Gln	
			980					985					990			
Cys	Gly	Val	Gly	Gln	Arg	Gln	Arg	Ser	Val	Arg	Cys	Thr	Ser	His	Thr	
		995						1000					1005			
Gly	Gln	Ala	Ser	His	Glu	Cys	Thr	Glu	Ala	Leu	Arg	Pro	Pro	Thr	Thr	
		1010				1015					1020					
Gln	Gln	Cys	Glu	Ala	Lys	Cys	Asp	Ser	Pro	Thr	Pro	Gly	Asp	Gly	Pro	
1025					1030					1035					1040	
Glu	Glu	Cys	Lys	Asp	Val	Asn	Lys	Val	Ala	Tyr	Cys	Pro	Leu	Val	Leu	

1045	1050	1055
Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys Lys		
1060	1065	1070
Thr Cys Gln Gly His		
1075		
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Met Pro Gly Gly Pro Ser Pro Arg Ser Pro Ala Pro Leu Leu Arg Pro		
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Leu Leu Leu Leu Leu Cys Ala Leu Ala Pro Gly Ala Pro Gly Pro Ala		
20 25 30		
Pro Gly Arg Ala Thr Glu Gly Arg Ala Ala Leu Asp Ile Val His Pro		
35 40 45		
Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr Glu Leu Trp Pro		
50 55 60		
Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg Asp Ala Pro Ala		
65 70 75 80		
Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg Phe Asn Leu Thr		
85 90 95		
Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser Glu Thr Arg Arg		
100 105 110		
Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His Thr Pro Ala Cys		
115 120 125		
His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu Gly Gly Leu Ala		
130 135 140		
Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe Gln Leu Ser Asn		
145 150 155 160		
Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro Ala Arg Pro Gly		
165 170 175		
His Ala Gln Pro His Val Val Tyr Lys Arg Gln Ala Pro Glu Arg Leu		
180 185 190		
Ala Gln Arg Gly Asp Ser Ser Ala Pro Ser Thr Cys Gly Val Gln Val		
195 200 205		
Tyr Pro Glu Leu Glu Ser Arg Arg Glu Arg Trp Glu Gln Arg Gln Gln		
210 215 220		



Trp	Arg	Arg	Pro	Arg	Leu	Arg	Arg	Leu	His	Gln	Arg	Ser	Val	Ser	Lys	225	230	235	240
Glu	Lys	Trp	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Ala	Lys	Met	Val	Glu	245	250	255	
Tyr	His	Gly	Gln	Pro	Gln	Val	Glu	Ser	Tyr	Val	Leu	Thr	Ile	Met	Asn	260	265	270	
Met	Val	Ala	Gly	Leu	Phe	His	Asp	Pro	Ser	Ile	Gly	Asn	Pro	Ile	His	275	280	285	
Ile	Thr	Ile	Val	Arg	Leu	Val	Leu	Leu	Glu	Asp	Glu	Glu	Glu	Asp	Leu	290	295	300	
Lys	Ile	Thr	His	His	Ala	Asp	Asn	Thr	Leu	Lys	Ser	Phe	Cys	Lys	Trp	305	310	315	320
Gln	Lys	Ser	Ile	Asn	Met	Lys	Gly	Asp	Ala	His	Pro	Leu	His	His	Asp	325	330	335	
Thr	Ala	Ile	Leu	Leu	Thr	Arg	Lys	Asp	Leu	Cys	Ala	Ala	Met	Asn	Arg	340	345	350	
Pro	Cys	Glu	Thr	Leu	Gly	Leu	Ser	His	Val	Ala	Gly	Met	Cys	Gln	Pro	355	360	365	
His	Arg	Ser	Cys	Ser	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Pro	Leu	Ala	Phe	370	375	380	
Thr	Val	Ala	His	Glu	Leu	Gly	His	Ser	Phe	Gly	Ile	Gln	His	Asp	Gly	385	390	395	400
Ser	Gly	Asn	Asp	Cys	Glu	Pro	Val	Gly	Lys	Arg	Pro	Phe	Ile	Met	Ser	405	410	415	
Pro	Gln	Leu	Leu	Tyr	Asp	Ala	Ala	Pro	Leu	Thr	Trp	Ser	Arg	Cys	Ser	420	425	430	
Arg	Gln	Tyr	Ile	Thr	Arg	Phe	Leu	Asp	Arg	Gly	Trp	Gly	Leu	Cys	Leu	435	440	445	
Asp	Asp	Pro	Pro	Ala	Lys	Asp	Ile	Ile	Asp	Phe	Pro	Ser	Val	Pro	Pro	450	455	460	
Gly	Val	Leu	Tyr	Asp	Val	Ser	His	Gln	Cys	Arg	Leu	Gln	Tyr	Gly	Ala	465	470	475	480
Tyr	Ser	Ala	Phe	Cys	Glu	Asp	Met	Asp	Asn	Val	Cys	His	Thr	Leu	Trp	485	490	495	
Cys	Ser	Val	Gly	Thr	Thr	Cys	His	Ser	Lys	Leu	Asp	Ala	Ala	Val	Asp	500	505	510	
Gly	Thr	Arg	Cys	Gly	Glu	Asn	Lys	Trp	Cys	Leu	Ser	Gly	Glu	Cys	Val	515	520	525	

Pro	Val	Gly	Phe	Arg	Pro	Glu	Ala	Val	Asp	Gly	Gly	Trp	Ser	Gly	Trp	
	530					535					540					
Ser	Ala	Trp	Ser	Ile	Cys	Ser	Arg	Ser	Cys	Gly	Met	Gly	Val	Gln	Ser	
545					550					555					560	
Ala	Glu	Arg	Gln	Cys	Thr	Gln	Pro	Thr	Pro	Lys	Tyr	Lys	Gly	Arg	Tyr	
				565					570					575		
Cys	Val	Gly	Glu	Arg	Lys	Arg	Phe	Arg	Leu	Cys	Asn	Leu	Gln	Ala	Cys	
			580					585					590			
Pro	Ala	Gly	Arg	Pro	Ser	Phe	Arg	His	Val	Gln	Cys	Ser	His	Phe	Asp	
		595					600					605				
Ala	Met	Leu	Tyr	Lys	Gly	Gln	Leu	His	Thr	Trp	Val	Pro	Val	Val	Asn	
	610					615					620					
Asp	Val	Asn	Pro	Cys	Glu	Leu	His	Cys	Arg	Pro	Ala	Asn	Glu	Tyr	Phe	
625					630					635					640	
Ala	Lys	Lys	Leu	Arg	Asp	Ala	Val	Val	Asp	Gly	Thr	Pro	Cys	Tyr	Gln	
				645					650					655		
Val	Arg	Ala	Ser	Arg	Asp	Leu	Cys	Ile	Asn	Gly	Ile	Cys	Lys	Asn	Val	
			660					665					670			
Gly	Cys	Asp	Phe	Glu	Ile	Asp	Ser	Gly	Ala	Met	Glu	Asp	Arg	Cys	Gly	
		675				680						685				
Val	Cys	His	Gly	Asn	Gly	Ser	Thr	Cys	His	Thr	Val	Ser	Gly	Thr	Phe	
	690					695					700					
Glu	Glu	Ala	Glu	Gly	Leu	Gly	Tyr	Val	Asp	Val	Gly	Leu	Ile	Pro	Ala	
705					710					715					720	
Gly	Ala	Arg	Glu	Ile	Arg	Ile	Gln	Glu	Val	Ala	Glu	Ala	Ala	Asn	Phe	
				725					730					735		
Leu	Ala	Leu	Arg	Ser	Glu	Asp	Pro	Glu	Lys	Tyr	Phe	Leu	Asn	Gly	Gly	
			740					745					750			
Trp	Thr	Ile	Gln	Trp	Asn	Gly	Asp	Tyr	Gln	Val	Ala	Gly	Thr	Thr	Phe	
		755					760					765				
Thr	Tyr	Ala	Arg	Arg	Gly	Asn	Trp	Glu	Asn	Leu	Thr	Ser	Pro	Gly	Pro	
	770					775					780					
Thr	Lys	Glu	Pro	Val	Trp	Ile	Gln	Val	Pro	Ala	Ser	Arg	Gly	Pro	Gly	
785					790					795					800	
Gly	Gly	Ser	Arg	Gly	Gly	Val	Pro	Arg	Pro	Ser	Thr	Leu	His	Gly	Arg	
				805					810					815		
Ser	Arg	Pro	Gly	Gly	Val	Ser	Pro	Gly	Ser	Val	Thr	Glu	Pro	Gly	Ser	
			820					825					830			

Glu	Pro	Gly	Pro	Pro	Ala	Ala	Ala	Ser	Thr	Ser	Val	Ser	Pro	Ser	Leu
		835					840					845			
Lys	Trp	Pro	Asn	Leu	Val	Ala	Ala	Val	His	Arg	Gly	Gly	Trp	Gly	Gln
		850				855					860				
Ala	Pro	Leu	Gly	Leu	Gly	Gly	Trp	Arg	Arg	His	Leu	Val	Leu	Met	Gly
865					870					875					880
Pro	Arg	Leu	Pro	Thr	Gln	Leu	Leu	Phe	Gln	Glu	Ser	Asn	Pro	Gly	Val
				885					890					895	
His	Tyr	Glu	Tyr	Thr	Ile	His	Arg	Glu	Ala	Gly	Gly	His	Asp	Glu	Val
			900					905					910		
Pro	Pro	Pro	Val	Phe	Ser	Trp	His	Tyr	Gly	Pro	Trp	Thr	Lys	Cys	Thr
		915					920					925			
Val	Thr	Cys	Gly	Arg	Gly	Glu	Lys	Trp	Gly	Arg	His	Ser	Pro	Thr	Cys
	930					935					940				
Arg	Gly	Leu	Val	Ser	Gly	Gln	Gly	His	Trp	Leu	Gln	Leu	Pro	Ala	His
945					950					955					960
Cys	Trp	Ala	Thr	Thr	Gly	Leu	Glu	Val	Cys	Phe	Ser	Glu	Pro	Gln	Phe
				965					970					975	
Ser	Ile	Cys	Glu	Met	Arg	Leu	Ala	Ile	Ala	Leu	Cys	Pro	Arg	Pro	Ala
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Gly	Arg	Val	His	Gly											
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Ala	Ile	Met	Asn	Ile	Val	Ala	Lys	Leu	Phe	Gln	Asp	Ser	Ser	Leu	Gly
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Ser	Thr	Val	Asn	Ile	Leu	Val	Thr	Arg	Leu	Ile	Leu	Leu	Thr	Glu	Asp
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Gln	Pro	Thr	Leu	Glu	Ile	Thr	His	His	Ala	Gly	Lys	Ser	Leu	Asp	Ser
	50					55					60				
Phe	Cys	Lys	Trp	Gln	Lys	Ser	Ile	Val	Asn	His	Ser	Gly	His	Gly	Asn
65					70					75					80
Ala	Ile	Pro	Glu	Asn	Gly	Val	Ala	Asn	His	Asp	Thr	Ala	Val	Leu	Ile
				85					90					95	

Thr	Arg	Tyr	Asp	Ile	Cys	Ile	Tyr	Lys	Asn	Lys	Pro	Cys	Gly	Thr	Leu	100	105	110
Gly	Leu	Ala	Pro	Val	Gly	Gly	Met	Cys	Glu	Arg	Glu	Arg	Ser	Cys	Ser	115	120	125
Val	Asn	Glu	Asp	Ile	Gly	Leu	Ala	Thr	Ala	Phe	Thr	Ile	Ala	His	Glu	130	135	140
Ile	Gly	His	Thr	Phe	Gly	Met	Asn	His	Asp	Gly	Val	Gly	Asn	Ser	Cys	145	150	155
Gly	Ala	Arg	Gly	Gln	Asp	Pro	Ala	Lys	Leu	Met	Ala	Ala	His	Ile	Thr	165	170	175
Met	Lys	Thr	Asn	Pro	Phe	Val	Trp	Ser	Ser	Cys	Ser	Arg	Asp	Tyr	Ile	180	185	190
Thr	Ser	Phe	Leu	Asp	Ser	Gly	Leu	Gly	Leu	Cys	Leu	Asn	Asn	Arg	Pro	195	200	205
Pro	Arg	Gln	Asp	Phe	Val	Tyr	Pro	Thr	Val	Ala	Pro	Gly	Gln	Ala	Tyr	210	215	220
Asp	Ala	Asp	Glu	Gln	Cys	Arg	Phe	Gln	His	Gly	Val	Lys	Ser	Arg	Gln	225	230	235
Cys	Lys	Tyr	Gly	Glu	Val	Cys	Ser	Glu	Leu	Trp	Cys	Leu	Ser	Lys	Ser	245	250	255
Asn	Arg	Cys	Ile	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	Gly	Thr	Leu	Cys	260	265	270
Gln	Thr	His	Thr	Ile	Asp	Lys	Gly	Trp	Cys	Tyr	Lys	Arg	Val	Cys	Val	275	280	285
Pro	Phe	Gly	Ser	Arg	Pro	Glu	Gly	Val	Asp	Gly	Ala	Trp	Gly	Pro	Trp	290	295	300
Thr	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	Ser	305	310	315
Ser	Ser	Arg	His	Cys	Asp	Ser	Pro	Arg	Pro	Thr	Ile	Gly	Gly	Lys	Tyr	325	330	335
Cys	Leu	Gly	Glu	Arg	Arg	Arg	His	Arg	Ser	Cys	Asn	Thr	Asp	Asp	Cys	340	345	350
Pro	Pro	Gly	Ser	Gln	Asp	Phe	Arg	Glu	Val	Gln	Cys	Ser	Glu	Phe	Asp	355	360	365
Ser	Ile	Pro	Phe	Arg	Gly	Lys	Phe	Tyr	Lys	Trp	Lys	Thr	Tyr	Arg	Gly	370	375	380
Gly	Gly	Val	Lys	Ala	Cys	Ser	Leu	Thr	Cys	Leu	Ala	Glu	Gly	Phe	Asn	385	390	395
																400		

Phe	Tyr	Thr	Glu	Arg	Ala	Ala	Ala	Val	Val	Asp	Gly	Thr	Pro	Cys	Arg	
				405					410					415		
Pro	Asp	Thr	Val	Asp	Ile	Cys	Val	Ser	Gly	Glu	Cys	Lys	His	Val	Gly	
			420					425					430			
Cys	Asp	Arg	Val	Leu	Gly	Ser	Asp	Leu	Arg	Glu	Asp	Lys	Cys	Arg	Val	
		435					440					445				
Cys	Gly	Gly	Asp	Gly	Ser	Ala	Cys	Glu	Thr	Ile	Glu	Gly	Val	Phe	Ser	
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Pro	Ala	Ser	Pro	Gly	Ala	Gly	Tyr	Glu	Asp	Val	Val	Trp	Ile	Pro	Lys	
465					470					475					480	
Gly	Ser	Val	His	Ile	Phe	Ile	Gln	Asp	Leu	Asn	Leu	Ser	Leu	Ser	His	
				485					490					495		
Leu	Ala	Leu	Lys	Gly	Asp	Gln	Glu	Ser	Leu	Leu	Leu	Glu	Gly	Leu	Pro	
			500					505					510			
Gly	Thr	Pro	Gln	Pro	His	Arg	Leu	Pro	Leu	Ala	Gly	Thr	Thr	Phe	Gln	
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Leu	Arg	Gln	Gly	Pro	Asp	Gln	Val	Gln	Ser	Leu	Glu	Ala	Leu	Gly	Pro	
	530					535					540					
Ile	Asn	Ala	Ser	Leu	Ile	Val	Met	Val	Leu	Ala	Arg	Thr	Glu	Leu	Pro	
545					550					555					560	
Ala	Leu	Arg	Tyr	Arg	Phe	Asn	Ala	Pro	Ile	Ala	Arg	Asp	Ser	Leu	Pro	
				565					570					575		
Pro	Tyr	Ser	Trp	His	Tyr	Ala	Pro	Trp	Thr	Lys	Cys	Ser	Ala	Gln	Cys	
			580					585					590			
Ala	Gly	Gly	Ser	Gln	Val	Gln	Ala	Val	Glu	Cys	Arg	Asn	Gln	Leu	Asp	
		595					600					605				
Ser	Ser	Ala	Val	Ala	Pro	His	Tyr	Cys	Ser	Ala	His	Ser	Lys	Leu	Pro	
		610				615					620					
Lys	Arg	Gln	Arg	Ala	Cys	Asn	Thr	Glu	Pro	Cys	Pro	Pro	Asp	Trp	Val	
625					630					635					640	
Val	Gly	Asn	Trp	Ser	Leu	Cys	Ser	Arg	Ser	Cys	Asp	Ala	Gly	Val	Arg	
				645					650					655		
Ser	Arg	Ser	Val	Val	Cys	Gln	Arg	Arg	Val	Ser	Ala	Ala	Glu	Glu	Lys	
			660					665					670			
Ala	Leu	Asp	Asp	Ser	Ala	Cys	Pro	Gln	Pro	Arg	Pro	Pro	Val	Leu	Glu	
		675					680					685				
Ala	Cys	His	Gly	Pro	Thr	Cys	Pro	Pro	Glu	Trp	Ala	Ala	Leu	Asp	Trp	
	690					695					700					

Ser Glu Cys Thr Pro Ser Cys Gly Pro Gly Leu Arg His Arg Val Val  
 705 710 715 720  
 Leu Cys Lys Ser Ala Asp His Arg Ala Thr Leu Pro Pro Ala His Cys  
 725 730 735  
 Ser Pro Ala Ala Lys Pro Pro Ala Thr Met Arg Cys Asn Leu Arg Arg  
 740 745 750  
 Cys Pro Pro Ala Arg Trp Val Ala Gly Glu Trp Gly Glu Cys Ser Ala  
 755 760 765  
 Gln Cys Gly Val Gly Gln Arg Gln Arg Ser Val Arg Cys Thr Ser His  
 770 775 780  
 Thr Gly Gln Ala Ser His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr  
 785 790 795 800  
 Thr Gln Gln Cys Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly  
 805 810 815  
 Pro Glu Glu Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val  
 820 825 830  
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 Lys Thr Cys His Gly His  
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<220>  
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 Glu Glu Phe Leu Thr Tyr Leu Glu His Tyr Gln Leu Thr Ile Pro Ile  
 35 40 45  
 Arg Val Asp Gln Asn Gly Ala Phe Leu Ser Phe Thr Val Lys Asn Asp  
 50 55 60  
 Lys His Ser Arg Arg Arg Arg Ser Met Asp Pro Ile Asp Pro Gln Gln  
 65 70 75 80

Ala	Val	Ser	Lys	Leu	Phe	Phe	Lys	Leu	Ser	Ala	Tyr	Gly	Lys	His	Phe	
				85					90					95		
His	Leu	Asn	Leu	Thr	Leu	Asn	Thr	Asp	Phe	Val	Ser	Lys	His	Phe	Thr	
			100					105					110			
Val	Glu	Tyr	Trp	Gly	Lys	Asp	Gly	Pro	Gln	Trp	Lys	His	Asp	Phe	Leu	
		115					120					125				
Asp	Asn	Cys	His	Tyr	Thr	Gly	Tyr	Leu	Gln	Asp	Gln	Arg	Ser	Thr	Thr	
		130				135					140					
Lys	Val	Ala	Leu	Ser	Asn	Cys	Val	Gly	Leu	His	Gly	Val	Ile	Ala	Thr	
145					150					155					160	
Glu	Asp	Glu	Glu	Tyr	Phe	Ile	Glu	Pro	Leu	Lys	Asn	Thr	Thr	Glu	Asp	
				165					170					175		
Ser	Lys	His	Phe	Ser	Tyr	Glu	Asn	Gly	His	Pro	His	Val	Ile	Tyr	Lys	
			180					185					190			
Lys	Ser	Ala	Leu	Gln	Gln	Arg	His	Leu	Tyr	Asp	His	Ser	His	Cys	Gly	
		195					200					205				
Val	Ser	Asp	Phe	Thr	Arg	Ser	Gly	Lys	Pro	Trp	Trp	Leu	Asn	Asp	Thr	
		210				215						220				
Ser	Thr	Val	Ser	Tyr	Ser	Leu	Pro	Ile	Asn	Asn	Thr	His	Ile	His	His	
225					230					235					240	
Arg	Gln	Lys	Arg	Ser	Val	Ser	Ile	Glu	Arg	Phe	Val	Glu	Thr	Leu	Val	
				245					250					255		
Val	Ala	Asp	Lys	Met	Met	Val	Gly	Tyr	His	Gly	Arg	Lys	Asp	Ile	Glu	
			260					265					270			
His	Tyr	Ile	Leu	Ser	Val	Met	Asn	Ile	Val	Ala	Lys	Leu	Tyr	Arg	Asp	
		275					280					285				
Ser	Ser	Leu	Gly	Asn	Val	Val	Asn	Ile	Ile	Val	Ala	Arg	Leu	Ile	Val	
		290				295					300					
Leu	Thr	Glu	Asp	Gln	Pro	Asn	Leu	Glu	Ile	Asn	His	His	Ala	Asp	Lys	
305					310					315					320	
Ser	Leu	Asp	Ser	Phe	Cys	Lys	Trp	Gln	Lys	Ser	Ile	Leu	Ser	His	Gln	
				325					330					335		
Ser	Asp	Gly	Asn	Thr	Ile	Pro	Glu	Asn	Gly	Ile	Ala	His	His	Asp	Asn	
			340					345					350			
Ala	Val	Leu	Ile	Thr	Arg	Tyr	Asp	Ile	Cys	Thr	Tyr	Lys	Asn	Lys	Pro	
		355					360					365				
Cys	Gly	Thr	Leu	Gly	Leu	Ala	Ser	Val	Ala	Gly	Met	Cys	Glu	Pro	Glu	
		370				375					380					

Arg	Ser	Cys	Ser	Ile	Asn	Glu	Asp	Ile	Gly	Leu	Gly	Ser	Ala	Phe	Thr	385	390	395	400
Ile	Ala	His	Glu	Ile	Val	His	Asn	Phe	Gly	Met	Asn	His	Asp	Gly	Ile	405	410	415	
Gly	Asn	Ser	Cys	Gly	Arg	Lys	Val	Met	Lys	Gln	Gln	Asn	Tyr	Gly	Ser	420	425	430	
Ser	His	Tyr	Cys	Glu	Tyr	Gln	Ser	Phe	Phe	Leu	Val	Cys	Leu	Gln	Ser	435	440	445	
Arg	Xaa	His	His	Gln	Leu	Phe	Arg	Glu	Val	Cys	Arg	Glu	Leu	Trp	Cys	450	455	460	
Leu	Ser	Lys	Ser	Asn	Arg	Cys	Val	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	465	470	475	480
Gly	Thr	Leu	Cys	Gln	Thr	Gly	Asn	Ile	Glu	Lys	Gly	Trp	Cys	Tyr	Gln	485	490	495	
Gly	Asp	Cys	Val	Pro	Phe	Gly	Thr	Trp	Pro	Gln	Ser	Ile	Asp	Gly	Gly	500	505	510	
Trp	Gly	Pro	Trp	Ser	Leu	Trp	Gly	Glu	Cys	Ser	Arg	Thr	Cys	Gly	Gly	515	520	525	
Gly	Val	Ser	Ser	Ser	Leu	Arg	His	Cys	Asp	Ser	Pro	Ala	Pro	Ser	Gly	530	535	540	
Gly	Gly	Lys	Tyr	Cys	Leu	Gly	Glu	Arg	Lys	Arg	Tyr	Arg	Ser	Cys	Asn	545	550	555	560
Thr	Asp	Pro	Cys	Pro	Leu	Gly	Ser	Arg	Asp	Phe	Arg	Glu	Lys	Gln	Cys	565	570	575	
Ala	Asp	Phe	Asp	Asn	Met	Pro	Phe	Arg	Gly	Lys	Tyr	Tyr	Asn	Trp	Lys	580	585	590	
Pro	Tyr	Thr	Gly	Gly	Gly	Val	Lys	Pro	Cys	Ala	Leu	Asn	Cys	Leu	Ala	595	600	605	
Glu	Gly	Tyr	Asn	Phe	Tyr	Thr	Glu	Arg	Ala	Pro	Ala	Val	Ile	Asp	Gly	610	615	620	
Thr	Gln	Cys	Asn	Ala	Asp	Ser	Leu	Asp	Ile	Cys	Ile	Asn	Gly	Glu	Cys	625	630	635	640
Lys	His	Val	Gly	Cys	Asp	Asn	Ile	Leu	Gly	Ser	Asp	Ala	Arg	Glu	Asp	645	650	655	
Arg	Cys	Arg	Val	Cys	Gly	Gly	Gly	Gly	Ser	Thr	Cys	Asp	Ala	Ile	Glu	660	665	670	
Gly	Phe	Phe	Asn	Asp	Ser	Leu	Pro	Arg	Gly	Gly	Tyr	Met	Glu	Val	Val	675	680	685	



Gln Ile Pro Arg Gly Ser Val His Ile Glu Val Arg Glu Val Ala Met  
 690 695 700  
 Ser Lys Asn Tyr Ile Ala Leu Lys Ser Glu Gly Asp Asp Tyr Tyr Ile  
 705 710 715 720  
 Asn Gly Ala Trp Thr Ile Asp Trp Pro Arg Lys Phe Asp Val Ala Gly  
 725 730 735  
 Thr Ala Phe His Tyr Lys Arg Pro Thr Asp Glu Pro Glu Ser Leu Glu  
 740 745 750  
 Ala Leu Gly Pro Thr Ser Glu Asn Leu Ile Val Met Val Leu Leu Gln  
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 Glu Gln Asn Leu Gly Ile Arg Tyr Lys Phe Asn Val Pro Ile Thr Arg  
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 785 790 795 800  
 Trp Ser Glu Cys Ser Ala Thr Cys Ala Gly Gly Lys Met Pro Thr Arg  
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 Gln Pro Thr Gln Arg Ala Arg Trp Arg Thr Lys His Ile Leu Ser Tyr  
 820 825 830  
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 Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg  
 35 40 45  
 Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln  
 50 55 60  
 Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val  
 65 70 75 80  
 Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu

85					90					95					
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Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met
		115					120					125			
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys
	130					135					140				
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His
145					150					155					160
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly
				165					170					175	
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr
			180					185					190		
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val
		195					200					205			
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile
	210					215					220				
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu
225					230					235					240
Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val
				245					250					255	
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu
			260					265					270		
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val
		275					280					285			
Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu
	290					295					300				
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp
305					310					315					320
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala
				325					330					335	
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val
			340					345					350		
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu
		355					360					365			
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro
	370					375					380				
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn

385					390					395				400	
Val	Val	Glu	Glu	Ser	Ala	Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile
				405					410					415	
Leu	Gly	Ser	Ala	Met	Gln	Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr
			420					425					430		
Gly	Cys	Gly	Glu	Gln	Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val
		435					440					445			
Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr	Pro	Glu	Ile	Lys	Ser
	450					455					460				
Lys	Ala	Ile	Gly	Tyr	Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr
465					470					475					480
Lys	His	Tyr	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg
				485					490					495	
Asn	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala
			500					505					510		
Gln	Ala	Arg	Ala	Tyr	Ile	Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala
		515					520					525			
Leu	Ile	Trp	Leu	Ser	Gln	Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser
	530					535					540				
Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu
545					550					555					560
Val	Thr	Leu	Ser	Ala	Tyr	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu
				565					570					575	
Thr	Val	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser
			580					585					590		
Ala	Trp	Lys	Thr	Ala	Gln	Glu	Gly	Asp	His	Gly	Ser	His	Val	Tyr	Thr
		595					600					605			
Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Asn	Gln	Asp	Lys
	610					615					620				
Arg	Lys	Glu	Val	Leu	Lys	Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp
625					630					635					640
Asn	Ser	Val	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly
				645					650					655	
His	Phe	Tyr	Glu	Pro	Gln	Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser
			660					665					670		
Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu
		675					680					685			
Asp	Leu	Thr	Ser	Ala	Thr	Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln

690	695	700
Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu 705 710 715 720		
His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys 725 730 735		
Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe 740 745 750		
Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro 755 760 765		
Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val 770 775 780		
Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu 785 790 795 800		
Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu 805 810 815		
Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr 820 825 830		
Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys Met Val 835 840 845		
Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser 850 855 860		
Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr 865 870 875 880		
Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu 885 890 895		
Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr 900 905 910		
Asp Tyr Tyr Glu Thr Gly Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro 915 920 925		
Cys Ser Lys Asp Leu Gly Asn Ala 930 935		

<210> 36

<211> 898

<212> PRT

<213> Homo sapiens

<400> 36

Arg	Leu	Leu	Ile	Tyr	Ala	Val	Leu	Pro	Thr	Gly	Asp	Val	Ile	Gly	Asp
1				5					10					15	

Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu  
 20 25 30  
 Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg  
 35 40 45  
 Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln  
 50 55 60  
 Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val  
 65 70 75 80  
 Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu  
 85 90 95  
 Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile  
 100 105 110  
 Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met  
 115 120 125  
 Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys  
 130 135 140  
 Ile Arg Lys Glu Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro  
 145 150 155 160  
 Glu Thr Trp Ile Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala  
 165 170 175  
 Glu Val Gly Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly  
 180 185 190  
 Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu Gly Ile Ser Ser Thr Ala  
 195 200 205  
 Ser Leu Arg Ala Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr  
 210 215 220  
 Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn  
 225 230 235 240  
 Tyr Leu Pro Lys Cys Ile Arg Val Ser Val Gln Leu Glu Ala Ser Pro  
 245 250 255  
 Ala Phe Leu Ala Val Pro Val Glu Lys Glu Gln Ala Pro His Cys Ile  
 260 265 270  
 Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys Ser  
 275 280 285  
 Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Gln  
 290 295 300  
 Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg Lys  
 305 310 315 320

Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu	Lys	325	330	335
Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Ser	Gly	Gly	Glu	Val	Ser	340	345	350
Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn	Val	Val	Glu	Glu	Ser	Ala	355	360	365
Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	370	375	380
Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	385	390	400
Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn	Glu	405	410	415
Thr	Gln	Gln	Leu	Thr	Pro	Glu	Val	Lys	Ser	Lys	Ala	Ile	Gly	Tyr	Leu	420	425	430
Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Lys	His	Tyr	Asp	Gly	Ser	435	440	445
Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg	Asn	Gln	Gly	Asn	Thr	Trp	450	455	460
Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala	Gln	Ala	Arg	Ala	Tyr	Ile	465	470	475
Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala	Leu	Ile	Trp	Leu	Ser	Gln	485	490	495
Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	Ser	Gly	Ser	Leu	Leu	Asn	500	505	510
Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu	Val	Thr	Leu	Ser	Ala	Tyr	515	520	525
Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu	Thr	Val	Thr	His	Pro	Val	530	535	540
Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser	Ala	Trp	Lys	Thr	Ala	Gln	545	550	555
Glu	Gly	Asp	His	Gly	Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	565	570	575
Ala	Phe	Ala	Leu	Ala	Gly	Asn	Gln	Asp	Lys	Arg	Lys	Glu	Val	Leu	Lys	580	585	590
Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp	Asn	Ser	Val	His	Trp	Glu	595	600	605
Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly	His	Phe	Tyr	Glu	Pro	Gln	610	615	620

Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser	Tyr	Val	Leu	Leu	Ala	Tyr	625	630	635	640
Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu	Asp	Leu	Thr	Ser	Ala	Thr	645	650	655	
Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln	Asn	Ala	Gln	Gly	Gly	Phe	660	665	670	
Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys	Tyr	675	680	685	
Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys	Ala	Ala	Gln	Val	Thr	Ile	690	695	700	
Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe	Gln	Val	Asp	Asn	Asn	Asn	705	710	715	720
Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro	Glu	Leu	Pro	Gly	Glu	Tyr	725	730	735	
Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	Tyr	Leu	Gln	Thr	Ser	Leu	740	745	750	
Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu	Phe	Pro	Phe	Ala	Leu	Gly	755	760	765	
Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu	Pro	Lys	Ala	His	Thr	Ser	770	775	780	
Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr	Gly	Ser	Arg	Ser	Ala	Ser	785	790	795	800
Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro	Leu	805	810	815	
Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	Asn	His	Val	Ser	Arg	Thr	820	825	830	
Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser	Asn	835	840	845	
Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu	Gln	Asp	Val	Pro	Val	Arg	850	855	860	
Asp	Leu	Lys	Pro	Ala	Ile	Val	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Thr	Asp	865	870	875	880
Glu	Phe	Ala	Ile	Ala	Glu	Tyr	Asn	Ala	Pro	Cys	Ser	Lys	Asp	Leu	Gly	885	890	895	
Asn	Ala																		

<210> 37  
<211> 936

<212> PRT

<213> Homo sapiens

<400> 37

Arg	Leu	Leu	Ile	Tyr	Ala	Val	Leu	Pro	Thr	Gly	Asp	Val	Ile	Gly	Asp
1				5					10					15	
Ser	Ala	Lys	Tyr	Asp	Val	Glu	Asn	Glu	Leu	Ala	Asn	Lys	Val	Asp	Leu
			20				25						30		
Ser	Phe	Ser	Pro	Ser	Gln	Ser	Leu	Pro	Ala	Ser	His	Ala	His	Leu	Arg
		35					40					45			
Val	Thr	Ala	Ala	Pro	Gln	Ser	Val	Cys	Ala	Leu	Arg	Ala	Val	Asp	Gln
	50					55					60				
Ser	Val	Leu	Leu	Met	Lys	Pro	Asp	Ala	Glu	Leu	Ser	Ala	Ser	Ser	Val
65					70					75					80
Tyr	Asn	Leu	Leu	Pro	Glu	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Pro	Leu
				85					90					95	
Asn	Asp	Gln	Asp	Asp	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile
		100						105					110		
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met
		115					120					125			
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys
	130					135					140				
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His
145					150					155					160
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly
				165					170					175	
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr
			180					185						190	
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val
		195					200					205			
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile
	210					215					220				
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu
225					230					235					240
Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val
				245					250					255	
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu
			260					265					270		
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val
		275					280					285			



Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu		
290						295					300						
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp		
305					310					315					320		
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala		
				325					330					335			
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val		
			340					345					350				
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu		
		355					360					365					
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro		
	370					375					380						
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn		
385					390					395					400		
Val	Val	Glu	Glu	Ser	Ala	Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile		
				405					410					415			
Leu	Gly	Ser	Ala	Met	Gln	Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr		
			420					425					430				
Gly	Cys	Gly	Glu	Glx	Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val		
		435					440					445					
Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr	Pro	Glu	Ile	Lys	Ser		
	450					455					460						
Lys	Ala	Ile	Gly	Tyr	Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr		
465					470					475					480		
Lys	His	Tyr	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg		
				485					490					495			
Asn	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala		
			500					505					510				
Gln	Ala	Arg	Ala	Tyr	Ile	Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala		
		515					520					525					
Leu	Ile	Trp	Leu	Ser	Gln	Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser		
	530					535					540						
Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu		
545					550					555					560		
Val	Thr	Leu	Ser	Ala	Tyr	Ile	Lys	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu		
				565					570					575			
Thr	Val	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser		
			580					585					590				



Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr  
 900 905 910

Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro  
 915 920 925

Cys Ser Lys Asp Leu Gly Asn Ala  
 930 935

<210> 38  
 <211> 931  
 <212> PRT  
 <213> Rattus norvegicus

<400> 38  
 Arg Leu Val Leu Tyr Ala Ile Leu Pro Asn Gly Glu Val Val Gly Asp  
 1 5 10 15

Thr Ala Lys Tyr Glu Ile Glu Asn Cys Leu Ala Asn Lys Val Asp Leu  
 20 25 30

Val Phe Arg Pro Asn Ser Gly Leu Pro Ala Thr Arg Ala Leu Leu Ser  
 35 40 45

Val Met Ala Ser Pro Gln Ser Leu Cys Gly Leu Arg Ala Val Asp Gln  
 50 55 60

Ser Val Leu Leu Met Lys Pro Glu Thr Glu Leu Ser Ala Ser Leu Ile  
 65 70 75 80

Tyr Asp Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gln Gly Ala  
 85 90 95

Asp Gln Arg Glu Glu Asp Thr Asn Gly Cys Val Lys Gln Asn Asp Thr  
 100 105 110

Tyr Ile Asn Gly Ile Leu Tyr Ser Pro Val Gln Asn Thr Asn Glu Glu  
 115 120 125

Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn  
 130 135 140

Ser Asn Ile Arg Lys Pro Lys Val Cys Glu Arg Leu Arg Asp Asn Lys  
 145 150 155 160

Gly Ile Pro Ala Ala Tyr His Leu Val Ser Gln Ser His Met Asp Ala  
 165 170 175

Phe Leu Glu Ser Ser Glu Ser Pro Thr Glu Thr Arg Arg Ser Tyr Phe  
 180 185 190

Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val Asp Ser Ala Gly Val  
 195 200 205

Ala Glu Val Glu Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala

210					215					220					
Gly	Ala	Phe	Cys	Leu	Ser	Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Val
225					230					235					240
Val	Gln	Phe	Gln	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro
				245					250					255	
Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu
			260					265					270		
Asn	Tyr	Leu	Pro	Thr	Cys	Ile	Arg	Val	Ala	Val	Gln	Leu	Glu	Ala	Ser
		275					280					285			
Pro	Asp	Phe	Leu	Ala	Ala	Pro	Glu	Glu	Lys	Glu	Gln	Arg	Ser	His	Cys
	290					295					300				
Ile	Cys	Met	Asn	Gln	Arg	His	Thr	Ala	Ser	Trp	Ala	Val	Ile	Pro	Lys
305					310					315					320
Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Asn	Ser
				325					330					335	
Lys	Glu	Leu	Cys	Gly	Asn	Glu	Val	Pro	Val	Val	Pro	Glu	Gln	Gly	Lys
			340					345					350		
Lys	Asp	Thr	Ile	Ile	Lys	Ser	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu
		355					360					365			
Asn	Glu	Val	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Met	Gly	Ala	Glu	Val
	370					375					380				
Ser	Glu	Leu	Ile	Ala	Leu	Lys	Leu	Pro	Ser	Asp	Val	Val	Glu	Glu	Ser
385					390					395					400
Ala	Arg	Ala	Ser	Val	Thr	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met
				405					410					415	
Gln	Asn	Thr	Gln	Asp	Leu	Leu	Lys	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln
			420					425					430		
Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn
		435					440					445			
Glu	Thr	Gln	Gln	Leu	Thr	Gln	Glu	Ile	Lys	Thr	Lys	Ala	Ile	Ala	Tyr
	450					455					460				
Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Lys	His	Arg	Asp	Gly
465					470					475					480
Ser	Tyr	Ser	Ala	Phe	Gly	Asp	Lys	Pro	Gly	Arg	Asn	His	Ala	Asn	Thr
				485					490					495	
Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Ser	Phe	Ala	Gln	Ala	Arg	Lys	Tyr
			500					505					510		
Ile	Phe	Ile	Asp	Glu	Val	His	Ile	Thr	Gln	Ala	Leu	Leu	Trp	Leu	Ser

515					520					525					
Gln	Gln	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	Ser	Gly	Ser	Leu	Leu
530						535					540				
Asn	Asn	Ala	Met	Lys	Gly	Gly	Val	Glu	Asp	Glu	Val	Thr	Leu	Ser	Ala
545					550					555					560
Tyr	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Met	Ser	Leu	Pro	Val	Thr	His	Pro
				565					570					575	
Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala
			580						585				590		
Arg	Gly	Gly	Ala	Gly	Gly	Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala
		595					600					605			
Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys
	610					615					620				
Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala	Arg	Gly	Gly	Ala	Gly	Gly	Ser	His
625					630					635					640
Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro
				645					650					655	
Gln	Ala	Thr	Ser	Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Val	Leu	Leu	Ala
			660					665					670		
Tyr	Leu	Thr	Thr	Glu	Pro	Ala	Pro	Thr	Gln	Glu	Asp	Leu	Thr	Ala	Ala
		675					680					685			
Met	Leu	Ile	Val	Lys	Trp	Leu	Thr	Lys	Gln	Gln	Asn	Ser	His	Gly	Gly
	690					695					700				
Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys
705					710					715					720
Tyr	Gly	Ser	Ala	Thr	Phe	Thr	Arg	Ala	Lys	Lys	Ala	Ala	Gln	Val	Thr
				725					730					735	
Ile	Arg	Ser	Ser	Gly	Thr	Phe	Ser	Thr	Lys	Phe	Gln	Val	Asn	Asn	Asn
			740					745					750		
Asn	Gln	Leu	Leu	Leu	Gln	Arg	Val	Thr	Leu	Pro	Thr	Val	Pro	Gly	Asp
		755					760					765			
Tyr	Thr	Val	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	Tyr	Leu	Gln	Thr	Ser
	770					775					780				
Leu	Lys	Tyr	Ser	Val	Leu	Pro	Arg	Glu	Glu	Glu	Phe	Pro	Phe	Ala	Val
785					790					795					800
Val	Val	Gln	Thr	Leu	Pro	Gly	Thr	Cys	Glu	Asp	Pro	Lys	Ala	His	Thr
				805					810					815	
Ser	Phe	Gln	Ile	Ser	Leu	Asn	Ile	Ser	Tyr	Thr	Gly	Ser	Arg	Ser	Glu

820					825					830					
Ser	Asn	Met	Ala	Ile	Ala	Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro
		835					840					845			
Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	Val	His	Val	Ser	Arg
	850					855					860				
Thr	Glu	Val	Ser	Asn	Asn	His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser
865						870					875				880
Asn	Gln	Thr	Val	Asn	Leu	Ser	Phe	Thr	Val	Gln	Gln	Asp	Ile	Pro	Ile
				885					890					895	
Arg	Asp	Leu	Lys	Pro	Ala	Val	Val	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Lys
			900					905						910	
Asp	Glu	Phe	Ala	Val	Ala	Lys	Tyr	Ser	Ala	Pro	Cys	Ser	Thr	Asp	Tyr
		915					920					925			
Gly	Asn	Ala													
		930													

<210> 39  
 <211> 941  
 <212> PRT  
 <213> Cavia porcellus

<400> 39															
Arg	Val	Leu	Ile	Tyr	Ala	Ile	Leu	Pro	Ser	Gly	Glu	Ile	Ile	Ala	Asp
1				5					10					15	
Ser	Ala	Lys	Tyr	Asn	Val	Glu	Asn	Cys	Leu	Asp	Asn	Lys	Val	Asn	Leu
			20					25					30		
Ser	Phe	Ser	Glu	Gly	Gln	Ser	Leu	Pro	Ala	Ser	Lys	Thr	His	Leu	Arg
		35					40					45			
Val	Thr	Ala	Ser	Pro	Gln	Ser	Leu	Cys	Ala	Leu	Arg	Ala	Val	Asp	Gln
	50					55					60				
Ser	Val	Leu	Leu	Arg	Lys	Pro	Glu	Ala	Val	Leu	Ser	Ala	Ser	Ser	Val
65					70					75					80
Tyr	Ala	Leu	Leu	Pro	Val	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Leu	Leu
				85					90					95	
Gly	Gln	Gln	Glu	Glu	Asn	Asp	Gly	Glu	Cys	Val	Ser	Leu	Tyr	Asn	Thr
			100					105					110		
Tyr	Ile	Asp	Gly	Ile	Leu	Tyr	Ser	Pro	Glu	Pro	Asn	Ile	Asn	Glu	Lys
		115					120					125			
Asp	Met	Tyr	Gly	Phe	Leu	Lys	Asp	Met	Gly	Leu	Lys	Val	Phe	Thr	Asn
	130					135					140				

Thr	Lys	Ile	Gln	Lys	Pro	Gln	Leu	Cys	Ala	His	Val	Gln	Lys	Phe	Glu	145	150	155	160
Val	Pro	Thr	Met	Ala	Tyr	Ser	Tyr	Ser	Glu	Ser	Ser	Ser	Phe	Arg	Ser	165	170	175	
Gly	Pro	Arg	Arg	Val	Pro	Ala	Val	Gly	Ile	Ala	Ala	Thr	Tyr	Ser	Glu	180	185	190	
Pro	Pro	Lys	Glu	Thr	Val	Arg	Thr	Tyr	Ser	Pro	Glu	Thr	Trp	Ile	Trp	195	200	205	
Asp	Leu	Lys	Val	Thr	Asp	Ser	Ser	Gly	Val	Ala	Glu	Val	Glu	Val	Thr	210	215	220	
Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	225	230	235	240
Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Thr	Ala	Ser	Leu	Arg	Ala	Phe	245	250	255	
Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	260	265	270	
Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Asp	Cys	275	280	285	
Ile	Arg	Ile	Ser	Val	His	Leu	Glu	Ala	Ser	Pro	Lys	Phe	Leu	Ala	Glu	290	295	300	
Pro	Lys	Ala	Lys	Glu	Gln	Glu	Ser	Tyr	Cys	Val	Cys	Gly	Asn	Glu	Arg	305	310	315	320
Gln	Thr	Val	Ser	Trp	Val	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	325	330	335	
Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Ser	Glu	Leu	Cys	Gly	Asn	340	345	350	
Glu	Lys	Thr	Val	Val	Pro	Thr	Tyr	Gly	Lys	Lys	Asp	Thr	Ile	Ile	Lys	355	360	365	
Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Ile	Glu	Lys	Glu	Glu	Thr	Trp	Thr	370	375	380	
Ser	Leu	Ile	Arg	Val	Ser	Asp	Thr	Thr	Val	Ser	Glu	Lys	Leu	His	Leu	385	390	395	400
Glu	Leu	Pro	Ser	Asn	Val	Ile	Gln	Asp	Ser	Ala	Arg	Ala	Thr	Val	Ser	405	410	415	
Ile	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	Asn	Ile	Gln	Asn	Leu	420	425	430	
Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	Met	Val	Leu	Phe	Ala	435	440	445	

76



Phe Ser Thr Asn Phe Glu Val Asn His Asn Asn Arg Leu Leu Leu Gln  
755 760 765  
Gln Val Ser Leu Pro Thr Val Ser Asp Ser Tyr Thr Ile Thr Val Thr  
770 775 780  
Gly Glu Gly Asn Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Val Pro  
785 790 795 800  
Ser Glu Lys Gly Thr Phe Pro Phe Ala Leu Glu Ala Glu Thr Val Pro  
805 810 815  
Gln Ala Cys Asp Gly Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu  
820 825 830  
Asn Val Ser Tyr Ile Gly Ser Arg Pro Val Ser Asn Met Ala Ile Val  
835 840 845  
Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys  
850 855 860  
Asn Leu Glu Lys Ser Glu His Ile Ser Arg Thr Glu Val Ser Asn Asn  
865 870 875 880  
His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu  
885 890 895  
Ser Phe Phe Val Val Gln Asp Ile Glu Val Arg Asp Leu Lys Pro Ala  
900 905 910  
Ile Ile Lys Val Tyr Asp Tyr Tyr Glu Thr Asn Glu Phe Ala Ile Ala  
915 920 925  
Glu Tyr His Ala Pro Cys Ser Lys Asp Pro Gly Asn Ala  
930 935 940

<210> 40  
<211> 373  
<212> PRT  
<213> Mus musculus

<400> 40  
Met Ser Thr Asp Cys Ala Gly Asn Ser Thr Cys Pro Val Asn Ser Thr  
1 5 10 15  
Glu Glu Asp Pro Pro Val Gly Met Glu Gly His Ala Asn Leu Lys Leu  
20 25 30  
Leu Phe Thr Val Leu Ser Ala Val Met Val Gly Leu Val Met Phe Ser  
35 40 45  
Phe Gly Cys Ser Val Glu Ser Gln Lys Leu Trp Leu His Leu Arg Arg  
50 55 60  
Pro Trp Gly Ile Ala Val Gly Leu Leu Ser Gln Phe Gly Leu Met Pro  
65 70 75 80

Leu Thr Ala Tyr Leu Leu Ala Ile Gly Phe Gly Leu Lys Pro Phe Gln  
 85 90 95  
 Ala Ile Ala Val Leu Met Met Gly Ser Cys Pro Gly Gly Thr Ile Ser  
 100 105 110  
 Asn Val Leu Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser  
 115 120 125  
 Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys  
 130 135 140  
 Leu Tyr Ile Tyr Thr Arg Ser Trp Thr Leu Thr Gln Asn Leu Val Ile  
 145 150 155 160  
 Pro Tyr Gln Ser Ile Gly Ile Thr Leu Val Ser Leu Val Val Pro Val  
 165 170 175  
 Ala Ser Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ala Thr Val  
 180 185 190  
 Ile Leu Lys Val Gly Ala Ile Leu Gly Gly Met Leu Leu Leu Val Val  
 195 200 205  
 Ala Val Thr Gly Met Val Leu Ala Lys Gly Trp Asn Thr Asp Val Thr  
 210 215 220  
 Leu Leu Val Ile Ser Cys Ile Phe Pro Leu Val Gly His Val Thr Gly  
 225 230 235 240  
 Phe Leu Leu Ala Phe Leu Thr His Gln Ser Trp Gln Arg Cys Arg Thr  
 245 250 255  
 Ile Ser Ile Glu Thr Gly Ala Gln Asn Ile Gln Leu Cys Ile Ala Met  
 260 265 270  
 Leu Gln Leu Ser Phe Ser Ala Glu Tyr Leu Val Gln Leu Leu Asn Phe  
 275 280 285  
 Ala Leu Ala Tyr Gly Leu Phe Gln Val Leu His Gly Leu Leu Ile Val  
 290 295 300  
 Ala Ala Tyr Gln Ala Tyr Lys Arg Arg Gln Lys Ser Lys Cys Arg Arg  
 305 310 315 320  
 Gln His Pro Asp Cys Pro Asp Val Cys Tyr Glu Lys Gln Pro Arg Glu  
 325 330 335  
 Thr Ser Ala Phe Leu Asp Lys Gly Asp Glu Ala Ala Val Thr Leu Gly  
 340 345 350  
 Pro Val Gln Pro Glu Gln His His Arg Ala Ala Glu Leu Thr Ser His  
 355 360 365  
 Ile Pro Ser Cys Glu  
 370

<210> 41  
 <211> 347  
 <212> PRT  
 <213> Oryzctolagus cuniculus

<400> 41

Met	Ser	Asn	Leu	Thr	Val	Gly	Cys	Leu	Ala	Asn	Ala	Thr	Val	Cys	Glu
1				5					10					15	
Gly	Ala	Ser	Cys	Val	Ala	Pro	Glu	Ser	Asn	Phe	Asn	Ala	Ile	Leu	Ser
			20					25					30		
Val	Val	Leu	Ser	Thr	Val	Leu	Thr	Ile	Leu	Leu	Ala	Leu	Val	Met	Phe
		35					40					45			
Ser	Met	Gly	Cys	Asn	Val	Glu	Ile	Lys	Lys	Phe	Leu	Gly	His	Ile	Arg
	50					55					60				
Arg	Pro	Trp	Gly	Ile	Phe	Ile	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met
65					70					75					80
Pro	Leu	Thr	Gly	Phe	Val	Leu	Ala	Val	Ala	Phe	Gly	Ile	Met	Pro	Ile
				85					90					95	
Gln	Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Ala
			100					105					110		
Ser	Asn	Ile	Leu	Ala	Tyr	Trp	Val	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val
		115					120					125			
Ser	Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu
	130					135					140				
Cys	Leu	Tyr	Val	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val
145					150					155					160
Ile	Pro	Tyr	Asp	Asn	Ile	Gly	Thr	Ser	Leu	Val	Ala	Leu	Val	Val	Pro
				165					170					175	
Val	Ser	Ile	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys
			180					185					190		
Ile	Ile	Leu	Lys	Val	Gly	Ser	Ile	Ala	Gly	Ala	Val	Leu	Ile	Val	Leu
		195					200					205			
Ile	Ala	Val	Val	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu
	210					215					220				
Pro	Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Met	Ala	Gly	Tyr	Ser
225					230					235					240
Leu	Gly	Phe	Phe	Leu	Ala	Arg	Ile	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys
				245					250					255	
Arg	Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser

260	265	270
Thr Ile Val Gln Leu Ser Phe	Ser Pro Glu Asp Leu	Thr Tyr Val Phe
275	280	285
Thr Phe Pro Leu Ile Tyr Ser	Ile Phe Gln Ile Ala	Phe Ala Ala Ile
290	295	300
Phe Leu Gly Ile Tyr Val Ala	Tyr Arg Lys Cys His Gly	Lys Asn Asp
305	310	315
Ala Glu Phe Pro Asp Ile Lys	Asp Thr Lys Thr Glu	Pro Glu Ser Ser
325	330	335
Phe His Gln Met Asn Gly Gly	Phe Gln Pro Glu	
340	345	

<210> 42  
 <211> 348  
 <212> PRT  
 <213> Rattus norvegicus

<400> 42
Met Asp Asn Ser Ser Val Cys Ser Pro Asn Ala Thr Phe Cys Glu Gly
1 5 10 15
Asp Ser Cys Leu Val Thr Glu Ser Asn Phe Asn Ala Ile Leu Ser Thr
20 25 30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
35 40 45
Met Gly Cys Asn Val Glu Ile Asn Lys Phe Leu Gly His Ile Lys Arg
50 55 60
Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
65 70 75 80
Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
85 90 95
Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
100 105 110
Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
115 120 125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
130 135 140
Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
145 150 155 160
Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
165 170 175

Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile  
 180 185 190  
 Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile  
 195 200 205  
 Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro  
 210 215 220  
 Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu  
 225 230 235 240  
 Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg  
 245 250 255  
 Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr  
 260 265 270  
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr  
 275 280 285  
 Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Ile Ile  
 290 295 300  
 Leu Gly Met Tyr Val Thr Tyr Lys Lys Cys His Gly Lys Asn Asp Ala  
 305 310 315 320  
 Glu Phe Leu Glu Lys Thr Asp Asn Asp Met Asp Pro Met Pro Ser Phe  
 325 330 335  
 Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys  
 340 345

<210> 43  
 <211> 348  
 <212> PRT  
 <213> Mus musculus

<400> 43  
 Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly  
 1 5 10 15  
 Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr  
 20 25 30  
 Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser  
 35 40 45  
 Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg  
 50 55 60  
 Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro  
 65 70 75 80  
 Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln  
 85 90 95

Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser  
 100 105 110  
 Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser  
 115 120 125  
 Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys  
 130 135 140  
 Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile  
 145 150 155 160  
 Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val  
 165 170 175  
 Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile  
 180 185 190  
 Ile Leu Lys Ile Gly Ser Ile Thr Gly Val Ile Leu Ile Val Leu Ile  
 195 200 205  
 Ala Val Ile Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro  
 210 215 220  
 Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu  
 225 230 235 240  
 Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg  
 245 250 255  
 Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr  
 260 265 270  
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr  
 275 280 285  
 Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Val Ile  
 290 295 300  
 Leu Gly Ile Tyr Val Thr Tyr Arg Lys Cys Tyr Gly Lys Asn Asp Ala  
 305 310 315 320  
 Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe  
 325 330 335  
 Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys  
 340 345

<210> 44

<211> 348

<212> PRT

<213> Mus musculus

<400> 44

Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly

1		5		10		15									
Asp	Ser	Cys	Val	Val	Pro	Glu	Ser	Asn	Phe	Asn	Ala	Ile	Leu	Asn	Thr
			20					25					30		
Val	Met	Ser	Thr	Val	Leu	Thr	Ile	Leu	Leu	Ala	Met	Val	Met	Phe	Ser
		35					40					45			
Met	Gly	Cys	Asn	Val	Glu	Val	His	Lys	Phe	Leu	Gly	His	Ile	Lys	Arg
	50					55					60				
Pro	Trp	Gly	Ile	Phe	Val	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met	Pro
65					70					75					80
Leu	Thr	Gly	Phe	Ile	Leu	Ser	Val	Ala	Ser	Gly	Ile	Leu	Pro	Val	Gln
				85					90					95	
Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Gly	Ser
			100					105					110		
Asn	Ile	Leu	Ala	Tyr	Trp	Ile	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val	Ser
		115					120					125			
Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys
	130					135					140				
Leu	Phe	Val	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val	Ile
145					150				155						160
Pro	Tyr	Asp	Ser	Ile	Gly	Ile	Ser	Leu	Val	Ala	Leu	Val	Ile	Pro	Val
				165					170					175	
Ser	Phe	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys	Ile
			180					185					190		
Ile	Leu	Lys	Ile	Gly	Ser	Ile	Thr	Gly	Val	Ile	Leu	Ile	Val	Leu	Ile
		195					200					205			
Ala	Val	Ile	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu	Pro
						215					220				
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ala	Gly	Tyr	Ser	Leu
225					230					235					240
Gly	Phe	Phe	Leu	Ala	Arg	Leu	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg
				245					250					255	
Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr
			260					265					270		
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr
		275					280					285			
Phe	Pro	Leu	Ile	Tyr	Thr	Val	Phe	Gln	Leu	Val	Phe	Ala	Ala	Val	Ile
	290					295					300				
Leu	Gly	Ile	Tyr	Val	Thr	Tyr	Arg	Lys	Cys	Tyr	Gly	Lys	Asn	Asp	Ala

305		310		315		320
Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe						
		325		330		335
Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys						
		340		345		
<210> 45						
<211> 348						
<212> PRT						
<213> Homo sapiens						
<400> 45						
Met Asp Asn Ser Ser Ile Cys Asn Pro Asn Ala Thr Ile Cys Glu Gly						
1		5		10		15
Asp Ser Cys Ile Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser Val						
		20		25		30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe Ser						
		35		40		45
Met Gly Cys Asn Val Glu Leu His Lys Phe Leu Gly His Leu Arg Arg						
		50		55		60
Pro Trp Gly Ile Val Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro						
		65		70		75
Leu Thr Gly Phe Val Leu Ser Val Ala Phe Gly Ile Leu Pro Val Gln						
		85		90		95
Ala Val Val Val Leu Ile Gln Gly Cys Cys Pro Gly Gly Thr Ala Ser						
		100		105		110
Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val Ser						
		115		120		125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys						
		130		135		140
Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile						
		145		150		155
Pro Tyr Asp Ser Ile Gly Thr Ser Leu Val Ala Leu Val Ile Pro Val						
		165		170		175
Ser Ile Gly Met Tyr Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile						
		180		185		190
Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile						
		195		200		205
Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Thr Ile Glu Pro						
		210		215		220



Lys Leu Trp Ile Ile Gly Thr Ile Tyr Pro Ile Ala Gly Tyr Gly Leu  
 225 230 235 240  
 Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys Arg  
 245 250 255  
 Thr Val Ala Leu Glu Thr Gly Leu Gln Asn Thr Gln Leu Cys Ser Thr  
 260 265 270  
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr  
 275 280 285  
 Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile Leu  
 290 295 300  
 Leu Gly Ala Tyr Val Ala Tyr Lys Lys Cys His Gly Lys Asn Asn Thr  
 305 310 315 320  
 Glu Leu Gln Glu Lys Thr Asp Asn Glu Met Glu Pro Arg Ser Ser Phe  
 325 330 335  
 Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys  
 340 345

<210> 46  
 <211> 272  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu  
 1 5 10 15  
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala  
 20 25 30  
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile  
 35 40 45  
 Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro  
 50 55 60  
 Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr  
 65 70 75 80  
 Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe  
 85 90 95  
 Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr Ser Ile Gly Glu  
 100 105 110  
 Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys  
 115 120 125  
 Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu  
 130 135 140

Leu	Val	Ser	Arg	Gln	Val	Ser	Asp	Asp	Leu	Thr	Glu	Arg	Ala	Ala	Thr
145					150					155					160
Phe	Gly	Leu	Ile	Leu	Asp	Asp	Val	Ser	Leu	Thr	His	Leu	Thr	Phe	Gly
				165					170					175	
Lys	Glu	Phe	Thr	Glu	Ala	Val	Glu	Ala	Lys	Gln	Val	Ala	Gln	Gln	Glu
			180					185					190		
Ala	Glu	Arg	Ala	Arg	Phe	Val	Val	Glu	Lys	Ala	Glu	Gln	Gln	Lys	Lys
		195					200					205			
Ala	Ala	Ile	Ile	Ser	Ala	Glu	Gly	Asp	Ser	Lys	Ala	Ala	Glu	Leu	Ile
	210					215					220				
Ala	Asn	Ser	Leu	Ala	Thr	Ala	Gly	Asp	Gly	Leu	Ile	Glu	Leu	Arg	Lys
225					230					235					240
Leu	Glu	Ala	Ala	Glu	Asp	Ile	Ala	Tyr	Gln	Leu	Ser	Arg	Ser	Arg	Asn
				245					250					255	
Ile	Thr	Tyr	Leu	Pro	Ala	Gly	Gln	Ser	Val	Leu	Leu	Gln	Leu	Pro	Gln
			260					265					270		

<210> 47  
 <211> 272  
 <212> PRT  
 <213> Rattus norvegicus

<400> 47

Met	Ala	Ala	Lys	Val	Phe	Glu	Ser	Ile	Gly	Lys	Phe	Gly	Leu	Ala	Leu
1				5					10					15	
Ala	Val	Ala	Gly	Gly	Val	Val	Asn	Ser	Ala	Leu	Tyr	Asn	Val	Asp	Ala
			20				25						30		
Gly	His	Arg	Ala	Val	Ile	Phe	Asp	Arg	Phe	Arg	Gly	Val	Gln	Asp	Ile
		35					40					45			
Val	Val	Gly	Glu	Gly	Thr	His	Phe	Leu	Ile	Pro	Trp	Val	Gln	Lys	Pro
	50					55					60				
Ile	Ile	Phe	Asp	Cys	Arg	Ser	Arg	Pro	Arg	Asn	Val	Pro	Val	Ile	Thr
65					70					75					80
Gly	Ser	Lys	Asp	Leu	Gln	Asn	Val	Asn	Ile	Thr	Leu	Arg	Ile	Leu	Phe
				85					90					95	
Arg	Pro	Val	Ala	Ser	Gln	Leu	Pro	Arg	Ile	Tyr	Thr	Ser	Ile	Gly	Glu
			100					105					110		
Asp	Tyr	Asp	Glu	Arg	Val	Leu	Pro	Ser	Ile	Thr	Thr	Glu	Ile	Leu	Lys

115					120					125						
Ser	Val	Val	Ala	Arg	Phe	Asp	Ala	Gly	Glu	Leu	Ile	Thr	Gln	Arg	Glu	
130					135					140						
Leu	Val	Ser	Arg	Gln	Val	Ser	Asp	Asp	Leu	Thr	Glu	Arg	Ala	Ala	Thr	
145					150					155					160	
Phe	Gly	Leu	Ile	Leu	Asp	Asp	Val	Ser	Leu	Thr	His	Leu	Thr	Phe	Gly	
					165					170					175	
Lys	Glu	Phe	Thr	Glu	Ala	Val	Glu	Ala	Lys	Gln	Val	Ala	Gln	Gln	Glu	
					180					185					190	
Ala	Glu	Arg	Ala	Arg	Phe	Val	Val	Glu	Lys	Ala	Glu	Gln	Gln	Lys	Lys	
					195					200					205	
Ala	Ala	Ile	Ile	Ser	Ala	Glu	Gly	Asp	Ser	Lys	Ala	Ala	Glu	Leu	Ile	
					210					215					220	
Ala	Asn	Ser	Leu	Ala	Thr	Ala	Gly	Asp	Gly	Leu	Ile	Glu	Leu	Arg	Lys	
225					230					235					240	
Leu	Glu	Ala	Ala	Glu	Asp	Ile	Ala	Tyr	Gln	Leu	Ser	Arg	Ser	Arg	Asn	
					245					250					255	
Ile	Thr	Tyr	Leu	Pro	Ala	Gly	Gln	Ser	Val	Leu	Leu	Gln	Leu	Pro	Gln	
					260					265					270	

<210> 48  
 <211> 1798  
 <212> PRT  
 <213> *Drosophila melanogaster*

<400> 48  
 Met Glu Met Arg Glu Val Leu Ser Arg Glu Gly Arg Glu Ala Lys Asn  
 1 5 10 15  
 Leu Leu Val Tyr Gln Phe Cys Asp Glu Thr Thr Ser Ser Gly Ala Thr  
 20 25 30  
 Ser Gly Phe Gly Ser Thr Gly Gly Asp Val Gly Gly Gly Ser Gly Gly  
 35 40 45  
 Asp Gly Pro Ala Val Gly Ser Gly Gly Val Leu Leu Asn Gly Asp Cys  
 50 55 60  
 Tyr Arg Lys Pro Pro Met Val Pro Pro Lys Ser Pro Asn Gly Thr Pro  
 65 70 75 80  
 Lys Asn Cys Gln Ser Pro Thr Ser Pro Arg Leu Lys Ser Ser Ala Ser  
 85 90 95

Val	Gly	Cys	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Pro	Arg	Val	Arg	Ser	Ala	100	105	110	
Ser	Thr	Gly	Arg	Asp	Lys	Lys	Ser	Glu	Leu	Gln	Ala	Arg	Tyr	Trp	Ala	115	120	125	
Leu	Leu	Phe	Gly	Asn	Leu	Gln	Arg	Ala	Ile	Asn	Glu	Ile	Tyr	Gln	Thr	130	135	140	
Val	Glu	Cys	Tyr	Glu	Asn	Ile	Ser	Ser	Cys	Gln	Glu	Thr	Ile	Leu	Val	145	150	155	160
Leu	Glu	Asn	Tyr	Val	Arg	Asp	Phe	Lys	Ala	Leu	Cys	Glu	Trp	Phe	Lys	165	170	175	
Val	Ser	Trp	Asp	Tyr	Glu	Ser	Arg	Pro	Leu	Gln	Gln	Arg	Pro	Gln	Ser	180	185	190	
Leu	Ala	Trp	Glu	Val	Arg	Lys	Ser	Asn	Pro	Thr	Pro	Arg	Val	Arg	Thr	195	200	205	
Arg	Ser	Leu	Cys	Ser	Pro	Asn	Asn	Ser	Gly	Lys	Ser	Ser	Pro	Ala	Leu	210	215	220	
Phe	Pro	Gly	Thr	Gln	Ser	Gly	Glu	Thr	Ser	Pro	Phe	Cys	Asp	Asn	Gly	225	230	235	240
Gln	Ile	Ser	Pro	Arg	Lys	Leu	Leu	Arg	Ala	Tyr	Asp	Gln	Val	Pro	Lys	245	250	255	
Gly	Ala	Met	Arg	Leu	Asn	Val	Arg	Glu	Leu	Phe	Ala	Ala	Ser	Lys	Arg	260	265	270	
Ala	Thr	Gln	Gly	Ser	Ser	Gln	Ser	Asp	Asn	Met	Glu	Gly	Pro	Leu	Asp	275	280	285	
Leu	Ser	Gly	Asp	Lys	Ser	Asn	Phe	Val	Leu	Arg	Ser	Thr	Gln	Tyr	Ala	290	295	300	
Gln	Thr	Asp	Leu	Glu	Asp	Pro	His	Leu	Thr	Leu	Ala	Asp	Val	Arg	Glu	305	310	315	320
Lys	Met	Arg	Met	Glu	Ala	Glu	Glu	Arg	Glu	Ala	Gln	Asn	Arg	Ile	Glu	325	330	335	
Asn	Glu	Ala	Leu	Glu	Glu	Val	Thr	Ile	Pro	Ile	Asp	Asn	Glu	Asp	Ala	340	345	350	
Thr	Glu	Ser	Leu	Asn	Lys	Gln	Glu	Pro	Ser	Ser	Leu	Glu	Leu	Pro	Ile	355	360	365	
His	Asn	Val	Ala	Asp	Leu	Ser	Lys	Glu	Pro	Glu	Leu	Met	Glu	Ala	Ala	370	375	380	
Ser	Glu	Ala	Thr	Ala	Leu	Glu	Met	Thr	Val	Ala	Ser	Leu	Glu	Ser	Met	385	390	395	400

Glu	Asn	Ala	Leu	Leu	Asn	Gln	Gln	Ala	Asn	Lys	Glu	Pro	Thr	Pro	Pro	
				405					410					415		
Ser	Thr	Val	Ile	Lys	Pro	Leu	Ala	Glu	Ile	Leu	Lys	Lys	Pro	Gln	Pro	
			420					425					430			
Leu	Asn	Pro	Leu	Ser	Gly	Asn	Asn	Val	Gln	Asn	Ser	Pro	Leu	Lys	Tyr	
		435					440					445				
Ser	Ser	Val	Leu	Asn	Arg	Pro	Ser	Lys	Lys	Met	Ile	Pro	Pro	Pro	Gly	
	450					455					460					
Gly	Val	Ala	Ala	Gln	Lys	Thr	Ile	Ser	Thr	Lys	Pro	Gly	Leu	Val	Lys	
465					470					475					480	
Pro	Asn	Leu	Thr	Thr	Thr	Val	Asn	Gly	Leu	Arg	Ser	Thr	Lys	Thr	Ala	
				485					490					495		
Thr	Ala	Pro	Pro	Ala	Ile	Lys	Thr	Thr	Gly	Arg	Ser	Gly	Leu	Gln	Arg	
			500					505					510			
His	Pro	Arg	Pro	Ser	Ser	Lys	Thr	Glu	Cys	Tyr	Gly	Pro	Pro	Asn	Asn	
		515					520					525				
Val	Ala	Ser	Arg	Leu	Ser	Ala	Arg	Ser	Arg	Thr	Ile	Asn	Thr	Leu	Lys	
	530					535					540					
Ala	Glu	Asn	Gln	His	Ser	Glu	Pro	Lys	Gln	Ile	Gln	Pro	Pro	Thr	Asp	
545					550					555					560	
Ala	Asp	Asp	Gly	Trp	Leu	Thr	Val	Lys	Asn	Arg	Arg	Arg	Thr	Ser	Met	
				565					570					575		
His	Trp	Ala	Asn	Arg	Phe	Asn	Gln	Pro	Thr	Gly	Tyr	Ala	Ser	Leu	Pro	
			580					585					590			
Thr	Leu	Ala	Leu	Leu	Asn	Glu	Gln	Gln	Lys	Glu	Gln	Glu	His	Lys	Glu	
		595					600					605				
Lys	Gln	Lys	Gly	Glu	Asp	Asp	Gly	Lys	Val	Ile	Val	Lys	Thr	Ile	Ser	
	610					615					620					
Ala	Lys	Thr	Lys	Ala	Pro	Ile	Glu	Val	Ala	Lys	Ala	Lys	Ala	Lys	Thr	
625					630					635					640	
Ser	Ile	Val	Ile	Thr	Arg	Pro	Glu	Ile	Lys	Asn	Ala	Lys	Ala	Lys	Val	
				645					650					655		
Asn	Ser	Phe	Pro	Val	Gln	Lys	Ser	Asn	Thr	Asn	Gln	Val	Lys	Lys	Pro	
			660					665					670			
Glu	Lys	Gln	Glu	Lys	Ser	Asp	Thr	Thr	Ala	Pro	Ala	Ala	Ile	Ala	Ser	
		675					680					685				
Ser	Arg	Leu	Lys	Met	Thr	Ser	Leu	His	Lys	Glu	Tyr	Met	Arg	Ser	Glu	
	690					695					700					

Lys	Asn	Ala	Leu	Arg	Lys	Leu	Gln	Gln	Lys	Glu	Gln	Gly	Asn	Gln	Gln	
705					710					715					720	
His	Asn	Ser	Ser	Ser	Ser	Ser	Ala	Glu	Thr	Val	Val	Glu	Ser	Cys	Asn	
				725					730					735		
Glu	Asp	His	Ser	Lys	Ile	Asp	Ile	Lys	Ile	Gln	Thr	Asn	Cys	Glu	Phe	
			740					745					750			
Ser	Lys	Thr	Ile	Gly	Glu	Leu	Tyr	Glu	Ser	Ile	Ala	His	Cys	Lys	Leu	
		755					760					765				
Pro	Ser	Gly	Ser	Leu	Lys	Thr	Asn	Ala	Ser	Thr	Leu	Ser	Ala	Cys	Asp	
	770					775					780					
Glu	Asn	Glu	Glu	Gln	Asn	Thr	Asp	Asp	Asn	Glu	Glu	Glu	Arg	Asn	Glu	
785					790					795					800	
Arg	Ile	Leu	Gly	Glu	Val	Gln	Glu	Ser	Leu	Glu	Arg	Gln	Ile	Arg	Glu	
				805					810					815		
Leu	Glu	Gln	Thr	Glu	Ile	Asp	Val	Asp	Thr	Glu	Thr	Asp	Glu	Thr	Asp	
			820					825					830			
Cys	Glu	Val	Gln	Leu	Glu	Glu	Gln	Asp	Asp	Gly	Val	Asp	Gly	Leu	Glu	
		835					840					845				
Met	Gly	Ser	Gly	Asp	Asp	Ser	Ala	Val	Phe	Val	Thr	Met	Ser	Asp	Asp	
	850					855					860					
Glu	Asn	Ala	Ser	Leu	Glu	Leu	Arg	Tyr	Gln	Ala	Leu	Leu	Ser	Asp	Met	
865					870					875					880	
Ser	Trp	Asn	Glu	Arg	Ala	Glu	Ala	Leu	Ala	Thr	Leu	Gln	Ala	Tyr	Val	
				885					890					895		
Ala	Arg	His	Pro	Gly	Arg	Ala	Gln	Glu	Leu	His	Gln	Lys	Leu	Ser	Ser	
			900					905					910			
Pro	Ser	Arg	Arg	Arg	Ser	Leu	Gln	Glu	Thr	Leu	Lys	Lys	Tyr	Gln	Ala	
		915					920					925				
Lys	Gln	Ala	Arg	Ala	Gln	Gln	Lys	Arg	Asn	Leu	Leu	Gln	Gln	Glu	Lys	
	930					935					940					
Ala	Ala	Lys	Leu	Gln	Gln	Leu	Phe	Ser	Arg	Val	Glu	Asp	Val	Lys	Ala	
945					950					955					960	
Ala	Lys	Asn	Gln	Ile	Ile	Glu	Asp	Lys	Arg	Gln	Lys	Met	Gln	Gly	Arg	
				965					970					975		
Leu	Gln	Arg	Ala	Ala	Glu	Asn	Arg	Glu	Gln	Tyr	Leu	Lys	Gln	Ile	Ile	
			980					985					990			
Glu	Lys	Ala	His	Asp	Glu	Glu	Lys	Lys	Leu	Lys	Glu	Ile	Asn	Phe	Ile	
		995					1000					1005				

Lys Asn Ile Glu Ala Gln Asn Lys Arg Leu Asp Leu Leu Glu Ser Ser  
 1010 1015 1020  
 Lys Glu Thr Glu Gly Arg Leu Gln Asp Leu Glu Gln Glu Arg Gln Lys  
 1025 1030 1035 1040  
 Arg Val Glu Glu Lys Leu Ala Lys Glu Ala Ala Val Glu Arg Arg Arg  
 1045 1050 1055  
 Gln Ala Leu Glu Lys Glu Arg Leu Leu Lys Leu Glu Lys Met Asn Glu  
 1060 1065 1070  
 Thr Arg Leu Glu Lys Glu Gln Arg Ile Gly Lys Met Gln Glu Gln Lys  
 1075 1080 1085  
 Glu Lys Gln Arg Gln Ala Leu Ala Arg Glu Lys Ala Arg Asp Arg Glu  
 1090 1095 1100  
 Glu Arg Leu Leu Ala Leu Gln Val Gln Gln Gln Gln Thr Thr Glu Glu  
 1105 1110 1115 1120  
 Leu Gln Arg Lys Ile Leu Gln Lys Gln Met Glu Ser Ala Arg Arg His  
 1125 1130 1135  
 Glu Glu Asn Ile Glu His Ile Arg Gln Arg Ala Leu Glu Leu Thr Ile  
 1140 1145 1150  
 Pro Thr Arg Gln Ala Asp Glu Gly Arg Gly Asp Gln Asp Val Ser Glu  
 1155 1160 1165  
 Asp Ile Leu Asn Gly Asn Ala Thr Ser Thr Thr Asn Glu Asp Cys Asp  
 1170 1175 1180  
 Leu Ser Ser Ser Leu Ser Glu Val Gly Gly Asn Asn Ala His Thr Arg  
 1185 1190 1195 1200  
 Ser Tyr Lys Lys Lys Met Lys Lys Leu Lys Gln Arg Met Asn Gln Cys  
 1205 1210 1215  
 Ala Ala Glu Tyr Leu Glu Ser Leu Glu Ala Leu Pro Ala His Ala Arg  
 1220 1225 1230  
 Arg Asp Ser Thr Val Pro Lys Leu Leu Asn Leu Val Val Lys Gly Gly  
 1235 1240 1245  
 Gly Ala Gln Gly Leu Asp Arg Asn Leu Gly Asn Leu Leu Arg Val Ile  
 1250 1255 1260  
 Pro Lys Ala Gln Thr Leu Asp Phe Leu Ala Phe Leu Cys Met Asp Gly  
 1265 1270 1275 1280  
 Leu Gly Ile Leu Ala Asn His Val Ile Ser Lys Gly Met Asp Glu Asn  
 1285 1290 1295  
 Ser Glu Ile Ser Arg Lys Ser Val Tyr Leu Ala Ala Gln Leu Tyr Arg  
 1300 1305 1310

Asn Ala Cys Ser Val Cys Pro Gln Ile Ala Arg His Ala Leu Leu Gly  
 1315 1320 1325  
 Asn Ser Ile Thr Val Leu Phe Asp Ala Ile Asn Lys Ser Phe Gln Val  
 1330 1335 1340  
 Ile Leu Lys Ser Asn Arg Cys Thr Lys Glu Thr Phe Ser Asn Phe Trp  
 1345 1350 1355 1360  
 Pro Pro Lys Met Leu His Asn Lys Ser Val Ala Arg Gln Ser Ser Arg  
 1365 1370 1375  
 Leu Glu Ala Leu Ser Leu Pro Glu Glu Lys Ser Pro Gln His Pro Val  
 1380 1385 1390  
 Glu Leu Ser Thr Glu Leu Met Leu Ala Cys Thr Glu Ala Leu Ser Ser  
 1395 1400 1405  
 Ser Tyr Val Lys Lys Asn Thr His Pro Lys Val Pro Glu Arg Leu Pro  
 1410 1415 1420  
 Asp Met Ile Asn Asp Cys Arg Phe His Trp Gln Asp Val Asn Lys Glu  
 1425 1430 1435 1440  
 Asp Met Leu Ala Asp Glu Phe Arg Lys Tyr Lys Cys Tyr Glu Lys Asn  
 1445 1450 1455  
 Pro Val Ile Ala Leu Pro His Pro Ser Leu Ser Ala Ser Leu Cys Arg  
 1460 1465 1470  
 Ser Leu Ser Ala Thr Pro Leu Lys Ile Asn Leu His Gln Phe Leu Gly  
 1475 1480 1485  
 Ser Gly Ile Leu Ile Leu Arg Leu Asn His His Arg His Pro Ala Thr  
 1490 1495 1500  
 Gly Ala Ser Phe Ser Asp Ser Cys Cys Thr Cys Cys Pro Lys Leu Thr  
 1505 1510 1515 1520  
 Thr Glu Ala Ala Val Ala Ala Val Ala Ala His Gln His Gln His Gln  
 1525 1530 1535  
 Asn Gln Gln Gln Gln Pro Asp Tyr Ala Val Ile Thr Gly Leu Ile Glu  
 1540 1545 1550  
 Ile Leu Ser Arg Arg Ile Gln Lys Val Arg Glu Ser Ile Glu Ser Asn  
 1555 1560 1565  
 Lys Ser Val Met Leu Ser Leu Leu Thr Thr Leu Gly Phe Leu Ser Arg  
 1570 1575 1580  
 Phe Ile Asp Val Cys Gln Pro Gly Pro Ala Asp Pro Thr Arg Leu Leu  
 1585 1590 1595 1600  
 Ser Ala Ala Lys Ser Thr Glu Leu Phe Gly Thr Val Ser Met Leu Tyr  
 1605 1610 1615



Gly Cys Val Met Pro Met Gly Glu Cys Ile Pro Pro Arg Thr Thr Ala  
 1620 1625 1630  
 Leu Ala Ala Ser Thr Phe His Leu Tyr Val Ser Leu Ala Ser Leu Asp  
 1635 1640 1645  
 Val Asn Thr Phe Gln Glu Thr Leu Thr Val Glu Gly Pro Leu Ser Leu  
 1650 1655 1660  
 Lys Leu Leu Asp Val Met Thr Val Ile Leu Asn Cys Ser Leu Val Asn  
 1665 1670 1675 1680  
 Asp Gln Trp Thr Thr Asn Ser Glu Ser Cys Pro Met Leu Ile Asp Leu  
 1685 1690 1695  
 Val Ala Ser Met Ala Phe Phe Cys Val Asn Asn Arg Arg His Gln Asp  
 1700 1705 1710  
 Leu Leu Ile Ser Glu Gln Tyr Ala Val Ile Phe Lys Arg Met Ala Lys  
 1715 1720 1725  
 Leu Pro Thr Gln Phe Asn Pro Val Ile Tyr Pro Phe Leu Val Thr Val  
 1730 1735 1740  
 Ser Phe Asn Asn Pro Pro Ala Arg Glu Phe Leu Ser Lys Asp Phe Asp  
 1745 1750 1755 1760  
 Leu Thr Phe Leu Asp Glu Tyr Ser Lys Ser Glu Met Ala Gln Arg Asn  
 1765 1770 1775  
 Val Val Ile Lys Leu Ile Asn Ser Arg Thr Lys Asp Lys Ile Ser Ala  
 1780 1785 1790  
 Gly Asn Lys Lys Asn Ala  
 1795

<210> 49

<211> 274

<212> PRT

<213> Toxocara canis

<400> 49

Met Ala Gly Ala Gln Lys Leu Leu Gly Arg Leu Gly Gln Ile Gly Val  
 1 5 10 15  
 Ala Leu Ala Val Thr Gly Gly Val Val Gln Ser Ala Leu Tyr Asn Val  
 20 25 30  
 Asp Gly Gly Gln Arg Ala Val Ile Phe Asp Arg Phe Thr Gly Val Lys  
 35 40 45  
 Pro Asp Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln  
 50 55 60  
 Arg Pro Ile Ile Phe Asp Ile Arg Ser Thr Pro Arg Ala Ile Ser Thr  
 65 70 75 80

Ile	Thr	Gly	Ser	Lys	Asp	Leu	Gln	Asn	Val	Ser	Ile	Thr	Leu	Arg	Ile	
				85					90					95		
Leu	His	Arg	Pro	Glu	Pro	Ser	Lys	Leu	Pro	Asn	Ile	Tyr	Leu	Asn	Ile	
			100					105					110			
Gly	Gln	Asp	Tyr	Ala	Glu	Arg	Val	Leu	Pro	Ser	Ile	Thr	Asn	Glu	Val	
		115					120					125				
Leu	Lys	Ala	Val	Val	Ala	Gln	Phe	Asp	Ala	His	Glu	Met	Ile	Thr	Gln	
	130					135					140					
Arg	Glu	Ser	Val	Ser	His	Arg	Val	Ser	Val	Glu	Leu	Ser	Glu	Arg	Ala	
145					150					155					160	
Arg	Gln	Phe	Gly	Ile	Leu	Leu	Asp	Asp	Ile	Ala	Ile	Thr	His	Leu	Ser	
				165					170					175		
Phe	Gly	Arg	Glu	Phe	Thr	Glu	Ala	Val	Glu	Met	Lys	Gln	Val	Ala	Gln	
			180					185					190			
Gln	Glu	Ala	Glu	Lys	Ala	Arg	Tyr	Leu	Val	Glu	Thr	Ala	Glu	Gln	Met	
		195					200					205				
Lys	Ile	Ala	Ala	Ile	Thr	Thr	Ala	Glu	Gly	Asp	Ala	Gln	Ala	Ala	Lys	
	210					215					220					
Leu	Leu	Ala	Gln	Ala	Phe	Lys	Asp	Ala	Gly	Asp	Gly	Leu	Ile	Glu	Leu	
225					230					235					240	
Arg	Lys	Ile	Glu	Ala	Ala	Glu	Glu	Ile	Ala	Glu	Arg	Met	Ser	Lys	Thr	
				245					250					255		
Arg	Asn	Val	Ile	Tyr	Leu	Pro	Gly	Asn	Gln	Asn	Thr	Leu	Phe	Asn	Leu	
		260						265					270			

Pro Ala

<210> 50

<211> 402

<212> PRT

<213> Caenorhabditis elegans

<400> 50

Met	Glu	Lys	Tyr	Lys	Asn	Glu	Leu	Glu	Ile	Phe	Lys	Arg	Met	Tyr	Phe	
1				5					10					15		

Lys	Asn	Tyr	Pro	Thr	Ser	Ser	Lys	Asp	Glu	Glu	Ala	Ala	Ala	Val	Ile	
			20					25					30			

Gln	Lys	Gly	Gly	Glu	Phe	Ile	Gln	Glu	Ile	Leu	Pro	Thr	Ile	Ile	Ser	
		35					40					45				

Thr	Ser	Arg	Ala	Tyr	Asp	Thr	Asn	Gln	Lys	Ala	Leu	Leu	Leu	Ala	Glu	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

50					55					60					
Gly 65	Gly	Lys	Met	Tyr	Asn 70	Val	Leu	Glu	Asp	Tyr 75	Asn	Glu	Thr	Ala	Glu 80
Lys	Met	Leu	Ser	Lys 85	Ser	Val	Arg	Met	Asn 90	Pro	Lys	Asn	Ala	Asp	Ala 95
Trp	His	Glu	Leu	Gly 100	Leu	Cys	Val	Met	Lys 105	Arg	Arg	Asp	Leu	Glu	Phe 110
Ala	Gln	Ser	Cys	Phe	Lys	Ile	Ala	Leu	Gly 120	Ile	Ser	Lys	Thr	Ala	Pro 125
Ile	Leu	Thr	Ser	Leu	Ala	Val 135	Ala	Met	Arg	Leu	Val 140	Ala	Leu	Glu	His
Pro 145	Glu	Pro	Ala	Gln	Ala	Glu 150	Ile	Arg	Thr	Lys 155	Ala	Met	Glu	Leu	Ile 160
Ile	Glu	Ala	Arg	Arg	Leu	Asp	Ser	Ala	Tyr 170	Gly	Pro	Ala	Asn	Ile	Ala 175
Phe	Ala	Thr	Gly 180	Leu	Phe	Tyr	Cys	Phe	Phe 185	Ser	Thr	Ala	Lys	Val	Glu 190
Leu	Lys	Phe	Leu	Asp	Lys	Val	Ile	Glu	Asn 200	Tyr	Lys	Lys	Ala	Leu	Glu 205
Cys	Glu	Leu	Ser	Arg	Thr	Asp 215	Pro	Gln	Val	Tyr 220	Ile	Asn	Met	Ala	Thr
Cys 225	Leu	Lys	Phe	Met	Glu	Lys 230	Tyr	Asp	Glu	Ala	Leu	Ala	Val	Leu	Gln 240
Lys	Ala	Val	Glu	Tyr 245	Asp	Pro	Arg	Asn	Glu 250	Leu	Glu	Thr	Arg	Glu	Lys 255
Leu	Ala	Ser	Phe	Val	Ser	Tyr	Leu	Ser 265	Lys	Phe	Thr	Asp	Ala	Ile	Gln 270
Lys	Lys	Gly 275	Lys	Met	Lys	Ala	Lys	Arg 280	Met	Gln	Glu	Met	Ile	Asn	Glu 285
Leu	Lys	Lys	Ser	Ser	Asp	Gly 295	Phe	Arg	Ala	Lys	Ile 300	Ile	Gly	Asn	Ile
Gly 305	His	Asp	Glu	Thr	Ile	Pro	Val	Ala	Leu	Val 315	Gly	Val	Asp	Ala	Ala 320
Gly	Glu	Val	Tyr	Gly 325	Ile	Thr	Ile	Tyr	Asn	Cys	Leu	Ser	Asn	Phe	Gly 335
Phe	Val	Ile	Gly	Asp	Thr	Val	Thr	Ile 345	Ala	Lys	Pro	Asp	Phe	Arg	Glu 350
Ile	Lys	Asn	Leu	Thr	Ile	Pro	Ser	Asp	Pro	Glu	Ile	His	Val	Asp	Ser

355		360		365
Val Lys Trp Ile Arg Val Ala Thr Pro Thr Gln Met Lys Lys Asn Gly				
370		375		380
Val Pro Leu Pro Glu Ser Val Leu Ala Arg Ala Val Ala Ser Thr Gln				
385		390		400
Thr Lys				
<210> 51				
<211> 711				
<212> PRT				
<213> Homo sapiens				
<400> 51				
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1		5		10
				15
Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr				
		20		25
				30
Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu				
		35		40
				45
Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met				
		50		55
				60
Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu				
		65		70
				75
Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly				
		85		90
				95
Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met				
		100		105
				110
Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly				
		115		120
				125
Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr				
		130		135
				140
Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro				
		145		150
				155
Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val				
		165		170
				175
Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val				
		180		185
				190
Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser				
		195		200
				205

Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro			
210						215					220							
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys			
225					230					235					240			
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro			
				245					250					255				
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala			
			260					265					270					
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly			
		275					280					285						
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys			
	290					295					300							
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu			
305					310					315					320			
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp			
				325					330					335				
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala			
			340					345					350					
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln			
		355					360					365						
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys			
	370					375					380							
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His			
385					390					395					400			
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu			
				405					410					415				
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr			
			420					425					430					
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys			
		435					440					445						
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln			
	450					455					460							
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser			
465					470					475					480			
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val			
				485					490					495				
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val			
			500					505					510					

Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His  
 515 520 525  
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn  
 530 535 540  
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met  
 545 550 555 560  
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg  
 565 570 575  
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu  
 580 585 590  
 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly  
 595 600 605  
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu  
 610 615 620  
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val  
 625 630 635 640  
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala  
 645 650 655  
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys  
 660 665 670  
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser  
 675 680 685  
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile  
 690 695 700  
 His Lys Val Met Arg Leu Gly  
 705 710

<210> 52  
 <211> 711  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val  
 1 5 10 15  
 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr  
 20 25 30  
 Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu  
 35 40 45  
 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met  
 50 55 60

Asp	Cys	Arg	Ala	Phe	His	Tyr	Asn	Val	Ser	Ser	His	Gly	Cys	Gln	Leu	65	70	75	80
Leu	Pro	Trp	Thr	Gln	His	Ser	Pro	His	Thr	Arg	Leu	Arg	Arg	Ser	Gly	85	90	95	
Arg	Cys	Asp	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met	100	105	110	
Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly	115	120	125	
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr	130	135	140	
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro	145	150	155	160
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val	165	170	175	
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val	180	185	190	
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser	195	200	205	
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	210	215	220	
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	225	230	235	240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	245	250	255	
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	260	265	270	
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	275	280	285	
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys	290	295	300	
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu	305	310	315	320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	325	330	335	
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	340	345	350	
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	355	360	365	

Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys	370	375	380	
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His	385	390	395	400
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu	405	410	415	
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	420	425	430	
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys	435	440	445	
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln	450	455	460	
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser	465	470	475	480
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val	485	490	495	
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val	500	505	510	
Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	His	515	520	525	
Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	Asn	530	535	540	
Pro	Gln	His	Gly	Glu	Pro	Ser	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	Met	545	550	555	560
Val	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	Arg	565	570	575	
Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	Glu	580	585	590	
Trp	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu	Ile	Ala	Gly	Trp	Gly	595	600	605	
Glu	Thr	Lys	Gly	Thr	Gly	Asn	Asp	Thr	Val	Leu	Asn	Val	Ala	Phe	Leu	610	615	620	
Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Ile	Lys	His	Arg	Gly	Arg	Val	625	630	635	640
Arg	Glu	Ser	Glu	Met	Cys	Thr	Glu	Gly	Leu	Leu	Ala	Pro	Val	Gly	Ala	645	650	655	
Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys	Phe	Thr	His	Asn	Cys	660	665	670	



Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser  
675 680 685

Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile  
690 695 700

His Lys Val Met Arg Leu Gly  
705 710

<210> 53

<211> 711

<212> PRT

<213> Homo sapiens

<400> 53

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Tyr Leu Gly Val  
1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr  
20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu  
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met  
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu  
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly  
85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met  
100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly  
115 120 125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr  
130 135 140

Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro  
145 150 155 160

Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val  
165 170 175

Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val  
180 185 190

Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser  
195 200 205

Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro

210					215					220					
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys
225					230					235					240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro
				245					250					255	
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala
			260					265					270		
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly
		275					280					285			
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys
	290					295					300				
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu
305					310					315					320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp
				325					330					335	
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala
			340					345					350		
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln
		355					360					365			
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys
	370					375					380				
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His
385					390					395					400
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu
				405					410					415	
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr
			420					425					430		
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys
		435					440					445			
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln
	450					455					460				
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser
465					470					475					480
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val
				485					490					495	
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val
			500					505					510		
Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	His

515					520					525					
Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	Asn
530						535					540				
Pro	Gln	His	Gly	Glu	Pro	Ser	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	Met
545					550					555					560
Val	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	Arg
				565					570					575	
Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	Glu
			580					585					590		
Trp	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu	Ile	Ala	Gly	Trp	Gly
		595					600					605			
Glu	Thr	Lys	Gly	Thr	Gly	Asn	Asp	Thr	Val	Leu	Asn	Val	Ala	Leu	Leu
						615					620				
Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Ile	Lys	His	Arg	Gly	Arg	Val
625					630					635					640
Arg	Glu	Ser	Glu	Met	Cys	Thr	Glu	Gly	Leu	Leu	Ala	Pro	Val	Gly	Ala
				645					650					655	
Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys	Phe	Thr	His	Asn	Cys
			660					665					670		
Trp	Val	Leu	Glu	Gly	Ile	Ile	Ile	Pro	Asn	Arg	Val	Cys	Ala	Arg	Ser
		675					680					685			
Arg	Trp	Pro	Ala	Val	Phe	Thr	Arg	Val	Ser	Val	Phe	Val	Asp	Trp	Ile
		690				695					700				
His	Lys	Val	Met	Arg	Leu	Gly									
705					710										

<210> 54  
 <211> 529  
 <212> PRT  
 <213> Homo sapiens

<400> 54  
 Met Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln  
 1 5 10 15  
 Leu Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg His Ser  
 20 25 30  
 Gly Arg Cys Asp Leu Phe Gln Glu Lys Asp Tyr Ile Arg Thr Cys Ile  
 35 40 45  
 Met Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly  
 50 55 60

Gly	Leu	Ser	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Gln	
65					70					75					80	
Tyr	Met	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	
				85					90					95		
Pro	Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	His	Thr	Thr	Asp	Pro	Ala	
			100					105					110			
Val	Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Val	Ala	Ala	Cys	
		115					120					125				
Val	Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	
	130					135					140					
Ser	Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	
145					150					155					160	
Pro	Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	
				165					170					175		
Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	
			180					185					190			
Pro	Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	
		195					200					205				
Ala	Gln	Pro	Arg	Gln	Glu	Ala	Thr	Ser	Val	Ser	Cys	Phe	Arg	Gly	Lys	
	210					215					220					
Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	
225					230					235					240	
Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	
				245					250					255		
Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	
			260					265					270			
Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	
		275					280					285				
Val	Gly	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	
	290					295					300					
Gln	Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	
305					310					315					320	
Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Gly	Ser	Ala	Glu	Thr	Pro	
				325					330					335		
His	Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	
			340					345					350			
Glu	Asn	Phe	Cys	Gln	Thr	Gln	Met	Gly	Ile	Ala	Met	Gly	Pro	Gly	Ala	
		355					360					365				

Thr	Arg	Trp	Thr	Gln	Gly	Pro	His	Ser	Thr	Thr	Val	Pro	Cys	Asp	Ala
370						375					380				
Ala	Leu	Met	Thr	Ser	Arg	His	Gln	Ser	Trp	Thr	Pro	Gln	Thr	Arg	Cys
385					390					395					400
Ser	Leu	Arg	Ser	Val	Ala	Arg	Gly	Trp	Ile	Gly	Trp	Ile	Ser	Val	Val
				405					410					415	
Pro	Ser	Cys	Ala	Trp	Leu	Gly	Ala	Ile	Arg	Ala	Thr	His	Pro	Gly	Gln
			420					425					430		
Ser	Ala	Cys	Gly	Ile	Gly	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu
		435					440					445			
Val	Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys
	450					455					460				
His	Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln
465					470					475					480
Asn	Pro	Gln	His	Gly	Glu	Pro	Gly	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys
				485					490					495	
Met	Leu	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu
			500					505					510		
Arg	Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro
		515					520					525			

Glu

<210> 55  
 <211> 716  
 <212> PRT  
 <213> Mus musculus

<400> 55															
Met	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Val	Gln	Cys	Ser	Arg	Ala
1				5					10					15	
Leu	Gly	Gln	Arg	Ser	Pro	Leu	Asn	Asp	Phe	Gln	Leu	Phe	Arg	Gly	Thr
			20					25					30		
Glu	Leu	Arg	Asn	Leu	Leu	His	Thr	Ala	Val	Pro	Gly	Pro	Trp	Gln	Glu
		35					40					45			
Asp	Val	Ala	Asp	Ala	Glu	Glu	Cys	Ala	Arg	Arg	Cys	Gly	Pro	Leu	Leu
	50					55					60				
Asp	Cys	Arg	Ala	Phe	His	Tyr	Asn	Met	Ser	Ser	His	Gly	Cys	Gln	Leu
65					70					75					80
Leu	Pro	Trp	Thr	Gln	His	Ser	Leu	His	Thr	Gln	Leu	Tyr	His	Ser	Ser
				85					90					95	

Leu	Cys	His	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met
			100					105					110		
Asp	Asn	Gly	Val	Ser	Tyr	Arg	Gly	Thr	Val	Ala	Arg	Thr	Ala	Gly	Gly
		115					120					125			
Leu	Pro	Cys	Gln	Ala	Trp	Ser	Arg	Arg	Phe	Pro	Asn	Asp	His	Lys	Tyr
	130					135					140				
Thr	Pro	Thr	Pro	Lys	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro
145					150					155					160
Asp	Gly	Asp	Pro	Arg	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asn	Arg	Ser	Val
				165					170					175	
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Thr	Cys	Arg	Glu	Ala	Val	Cys	Val
			180					185					190		
Leu	Cys	Asn	Gly	Glu	Asp	Tyr	Arg	Gly	Glu	Val	Asp	Val	Thr	Glu	Ser
		195					200					205			
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Ser	His	Pro
	210					215					220				
Phe	Gln	Pro	Glu	Lys	Phe	Leu	Asp	Lys	Asp	Leu	Lys	Asp	Asn	Tyr	Cys
225					230					235					240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro
				245					250					255	
Asn	Val	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Ser	Cys	Gly	Pro	Asn	Leu
			260					265					270		
Pro	Pro	Thr	Val	Lys	Gly	Ser	Lys	Ser	Gln	Arg	Arg	Asn	Lys	Gly	Lys
		275					280					285			
Ala	Leu	Asn	Cys	Phe	Arg	Gly	Lys	Gly	Glu	Asp	Tyr	Arg	Gly	Thr	Thr
	290					295					300				
Asn	Thr	Thr	Ser	Ala	Gly	Val	Pro	Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ser
305					310					315					320
Pro	His	Gln	His	Arg	Phe	Val	Pro	Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu
				325					330					335	
Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys
			340					345					350		
Phe	Thr	Ser	Arg	Pro	Gly	Leu	Arg	Met	Ala	Phe	Cys	His	Gln	Ile	Pro
		355					360					365			
Arg	Cys	Thr	Glu	Glu	Leu	Val	Pro	Glu	Gly	Cys	Tyr	His	Gly	Ser	Gly
	370					375					380				
Glu	Gln	Tyr	Arg	Gly	Ser	Val	Ser	Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys
385					390					395					400

Gln	His	Trp	Ser	Ser	Glu	Thr	Pro	His	Lys	Pro	Gln	Phe	Thr	Pro	Thr			
				405					410					415				
Ser	Ala	Pro	Gln	Ala	Gly	Leu	Glu	Ala	Asn	Phe	Cys	Arg	Asn	Pro	Asp			
			420					425					430					
Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	Thr	Leu	Asp	Pro	Asp	Ile	Leu			
		435					440					445						
Phe	Asp	Tyr	Cys	Ala	Leu	Gln	Arg	Cys	Asp	Asp	Asp	Gln	Pro	Pro	Ser			
	450					455					460							
Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Val	Phe	Glu	Lys	Cys	Gly	Lys	Arg			
465					470					475					480			
Val	Asp	Lys	Ser	Asn	Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn			
				485					490					495				
Ser	Pro	Trp	Thr	Val	Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys			
			500					505					510					
Gly	Gly	Ser	Leu	Val	Lys	Glu	Gln	Trp	Val	Leu	Thr	Ala	Arg	Gln	Cys			
		515					520					525						
Ile	Trp	Ser	Cys	His	Glu	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly			
	530					535					540							
Thr	Ile	Asn	Gln	Asn	Pro	Gln	Pro	Gly	Glu	Ala	Asn	Leu	Gln	Arg	Val			
545					550					555					560			
Pro	Val	Ala	Lys	Ala	Val	Cys	Gly	Pro	Ala	Gly	Ser	Gln	Leu	Val	Leu			
				565					570					575				
Leu	Lys	Leu	Glu	Arg	Pro	Val	Ile	Leu	Asn	His	His	Val	Ala	Leu	Ile			
			580					585					590					
Cys	Leu	Pro	Pro	Glu	Gln	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu			
		595					600					605						
Ile	Ala	Gly	Trp	Gly	Glu	Ser	Ile	Gly	Thr	Ser	Asn	Asn	Thr	Val	Leu			
	610					615					620							
His	Val	Ala	Ser	Met	Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Thr	Lys			
625					630					635					640			
Tyr	Arg	Gly	His	Ile	Gln	Glu	Ser	Glu	Ile	Cys	Thr	Gln	Gly	Leu	Val			
				645					650					655				
Val	Pro	Val	Gly	Ala	Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys			
			660					665					670					
Tyr	Thr	His	Asp	Cys	Trp	Val	Leu	Gln	Gly	Leu	Ile	Ile	Pro	Asn	Arg			
			675				680					685						
Val	Cys	Ala	Arg	Pro	Arg	Trp	Pro	Ala	Ile	Phe	Thr	Arg	Val	Ser	Val			
	690					695					700							

Phe Val Asp Trp Ile Asn Lys Val Met Gln Leu Glu  
 705 710 715

<210> 56  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser  
 1 5 10 15  
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu  
 20 25 30  
 Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Val Thr Cys Asp  
 35 40 45  
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln  
 50 55 60  
 Phe Ser Cys Pro Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly  
 65 70 75 80  
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln  
 85 90 95  
 His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys  
 100 105 110  
 Asp Gly Lys Leu Val Val Glu Cys Val Met Asn His Val Ala Cys Thr  
 115 120 125  
 Arg Ile Tyr Glu Lys Val Glu  
 130 135

<210> 57  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 57  
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser  
 1 5 10 15  
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu  
 20 25 30  
 Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp  
 35 40 45  
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln  
 50 55 60



Phe	Ser	Cys	Thr	Leu	Gly	Glu	Lys	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly
65					70					75					80
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
				85					90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Ser	Thr	Ile	Thr	Arg	Lys	Leu	Lys
			100					105					110		
Asp	Gly	Lys	Leu	Val	Val	Glu	Cys	Val	Met	Asn	Asn	Val	Thr	Cys	Thr
		115					120					125			
Arg	Ile	Tyr	Glu	Lys	Val	Glu									
	130					135									

<210> 58  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 58															
Met	Ala	Thr	Val	Gln	Gln	Leu	Glu	Gly	Arg	Trp	Arg	Leu	Val	Asp	Ser
1				5					10					15	
Arg	Gly	Phe	Asp	Glu	Tyr	Val	Lys	Glu	Leu	Gly	Val	Gly	Ile	Ala	Leu
			20					25					30		
Arg	Lys	Met	Asp	Thr	Ile	Ala	Lys	Pro	Asp	Cys	Ile	Ile	Thr	Cys	Asp
		35					40					45			
Gly	Lys	Asn	Leu	Thr	Ile	Lys	Thr	Glu	Ser	Thr	Leu	Lys	Thr	Thr	Gln
	50					55					60				
Phe	Ser	Cys	Thr	Leu	Gly	Glu	Asn	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly
65					70					75					80
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
				85					90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Asn	Thr	Ile	Arg	Arg	Lys	Leu	Lys
			100					105					110		
Asp	Gly	Lys	Leu	Val	Val	Asp	Cys	Val	Met	Asn	Ser	Val	Thr	Cys	Thr
		115					120					125			
Arg	Ile	Tyr	Glu	Lys	Val	Glu									
	130					135									

<210> 59  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 59															
Met	Ala	Thr	Val	Gln	Gln	Leu	Glu	Gly	Arg	Trp	Arg	Leu	Leu	Asp	Ser

1		5		10		15									
Lys	Gly	Phe	Asp	Glu	Tyr	Met	Lys	Glu	Leu	Gly	Val	Gly	Ile	Ala	Leu
			20					25					30		
Gln	Lys	Met	Gly	Ala	Met	Ala	Lys	Pro	Asp	Cys	Ile	Ile	Thr	Cys	Asp
		35						40				45			
Gly	Arg	Asn	Leu	Thr	Thr	Lys	Thr	Glu	Ser	Thr	Leu	Lys	Thr	Thr	Gln
	50					55					60				
Phe	Ser	Cys	Thr	Leu	Gly	Asp	Glu	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly
65					70				75						80
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
				85					90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Ser	Thr	Ile	Thr	Arg	Lys	Leu	Lys
			100					105					110		
Asp	Gly	Lys	Leu	Val	Val	Glu	Cys	Val	Met	Asn	Asn	Val	Thr	Cys	Thr
		115						120				125			
Arg	Ile	Tyr	Glu	Lys	Val	Glu									
	130					135									

<210> 60  
 <211> 135  
 <212> PRT  
 <213> Bos taurus

<400> 60
Met Ala Thr Val Gln Gln Leu Val Gly Arg Trp Arg Leu Val Glu Ser
1 5 10 15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Val Gly Val Gly Met Ala Leu
20 25 30
Arg Lys Val Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Ser Asp
35 40 45
Gly Lys Asn Leu Ser Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60
Phe Ser Cys Lys Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Glu
100 105 110
Asp Gly Lys Leu Val Val Val Cys Val Met Asn Asn Val Thr Cys Thr
115 120 125

Arg Val Tyr Glu Lys Val Glu  
130 135

<210> 61  
<211> 266  
<212> PRT  
<213> Homo sapiens

<400> 61  
Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15  
Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg  
20 25 30  
Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln  
35 40 45  
Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys  
50 55 60  
Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
65 70 75 80  
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95  
Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn  
100 105 110  
Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp  
115 120 125  
Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly  
130 135 140  
Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg  
145 150 155 160  
Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr  
165 170 175  
Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr  
180 185 190  
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu  
195 200 205  
Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro  
210 215 220  
Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser  
225 230 235 240  
Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly  
245 250 255

Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro  
260 265

<210> 62  
<211> 265  
<212> PRT  
<213> Rattus norvegicus

<400> 62

Met	Asn	Trp	Gly	Phe	Leu	Gln	Gly	Ile	Leu	Ser	Gly	Val	Asn	Lys	Tyr
1				5					10					15	
Ser	Thr	Ala	Leu	Gly	Arg	Ile	Trp	Leu	Ser	Val	Val	Phe	Ile	Phe	Arg
			20					25					30		
Val	Leu	Val	Tyr	Val	Val	Ala	Ala	Glu	Glu	Val	Trp	Asp	Asp	Glu	Gln
		35					40					45			
Lys	Asp	Phe	Ile	Cys	Asn	Thr	Lys	Gln	Pro	Gly	Cys	Pro	Asn	Val	Cys
	50					55					60				
Tyr	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
	65				70					75					80
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
				85					90					95	
Tyr	Arg	Glu	Glu	Arg	Glu	Arg	Lys	His	Arg	Leu	Lys	His	Gly	Pro	Asp
			100					105					110		
Ala	Pro	Ala	Leu	Tyr	Ser	Asn	Leu	Ser	Lys	Lys	Arg	Gly	Gly	Leu	Trp
		115					120					125			
Trp	Thr	Tyr	Leu	Leu	Ser	Leu	Ile	Phe	Lys	Ala	Ala	Val	Asp	Ser	Gly
	130					135					140				
Phe	Leu	Tyr	Ile	Phe	His	Cys	Ile	Tyr	Lys	Asp	Tyr	Asp	Met	Pro	Arg
145					150					155					160
Val	Val	Ala	Cys	Ser	Val	Gln	Pro	Cys	Pro	His	Thr	Val	Asp	Cys	Tyr
				165					170					175	
Ile	Ser	Arg	Pro	Thr	Glu	Lys	Lys	Val	Phe	Thr	Tyr	Phe	Met	Val	Val
			180					185					190		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Ser	Glu	Val	Ala	Tyr	Leu
		195					200					205			
Val	Gly	Lys	Arg	Cys	Met	Glu	Val	Phe	Arg	Pro	Arg	Arg	Gln	Lys	Thr
	210					215					220				
Ser	Arg	Arg	His	Gln	Leu	Pro	Asp	Thr	Cys	Pro	Pro	Tyr	Val	Ile	Ser
225					230					235					240
Lys	Gly	His	Pro	Gln	Asp	Glu	Ser	Thr	Val	Leu	Thr	Lys	Ala	Gly	Met

245										250					255				
Ala	Thr	Val	Asp	Ala	Gly	Val	Tyr	Pro											
			260					265											
<210> 63																			
<211> 266																			
<212> PRT																			
<213> Mus musculus																			
<400> 63																			
Met	Asn	Trp	Gly	Phe	Leu	Gln	Gly	Ile	Leu	Ser	Gly	Val	Asn	Lys	Tyr				
1				5					10					15					
Ser	Thr	Ala	Leu	Gly	Arg	Ile	Trp	Leu	Ser	Val	Val	Phe	Ile	Phe	Arg				
			20					25					30						
Val	Leu	Val	Tyr	Val	Val	Ala	Ala	Glu	Glu	Val	Trp	Asp	Asp	Asp	Gln				
		35					40					45							
Lys	Asp	Phe	Ile	Cys	Asn	Thr	Lys	Gln	Pro	Gly	Cys	Pro	Asn	Val	Cys				
	50					55					60								
Tyr	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln				
65					70				75						80				
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala				
				85					90					95					
Tyr	Arg	Glu	Glu	Arg	Glu	Arg	Lys	His	Arg	Leu	Lys	His	Gly	Pro	Asn				
			100					105					110						
Ala	Pro	Ala	Leu	Tyr	Ser	Asn	Leu	Ser	Lys	Lys	Arg	Gly	Gly	Leu	Trp				
		115					120					125							
Trp	Thr	Tyr	Leu	Leu	Ser	Leu	Ile	Phe	Lys	Ala	Ala	Val	Asp	Ser	Gly				
		130				135					140								
Phe	Leu	Tyr	Ile	Phe	His	Cys	Ile	Tyr	Lys	Asp	Tyr	Asp	Met	Pro	Arg				
145					150				155					160					
Val	Val	Ala	Cys	Ser	Val	Thr	Pro	Cys	Pro	His	Thr	Val	Asp	Cys	Tyr				
			165					170						175					
Ile	Ala	Arg	Pro	Thr	Glu	Lys	Lys	Val	Phe	Thr	Tyr	Phe	Met	Val	Val				
			180					185					190						
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Ser	Glu	Val	Val	Tyr	Leu				
		195				200						205							
Val	Gly	Lys	Arg	Cys	Met	Glu	Val	Phe	Arg	Pro	Arg	Arg	Arg	Lys	Ala				
	210					215					220								
Ser	Arg	Arg	His	Gln	Leu	Pro	Asp	Thr	Cys	Pro	Pro	Tyr	Val	Ile	Ser				
225					230					235					240				

Lys Gly Gly His Pro Gln Asp Glu Ser Val Ile Leu Thr Lys Ala Gly  
245 250 255

Met Ala Thr Val Asp Ala Gly Val Tyr Pro  
260 265

<210> 64  
<211> 273  
<212> PRT  
<213> Homo sapiens

<400> 64  
Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg  
20 25 30

Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His  
35 40 45

Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys  
50 55 60

Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn  
100 105 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala  
130 135 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro  
145 150 155 160

Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe  
165 170 175

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala  
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu  
195 200 205

Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala  
210 215 220

Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln  
225 230 235 240

Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His  
245 250 255

Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile  
260 265 270

Leu

<210> 65  
<211> 273  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (41)  
<223> Wherein Xaa is any amino acid.

<400> 65  
Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg  
20 25 30

Val Leu Val Tyr Leu Val Thr Ala Xaa Arg Val Trp Ser Asp Asp His  
35 40 45

Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys  
50 55 60

Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn  
100 105 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala  
130 135 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro  
145 150 155 160

Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe  
165 170 175

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala  
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu  
 195 200 205  
 Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala  
 210 215 220  
 Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln  
 225 230 235 240  
 Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His  
 245 250 255  
 Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile  
 260 265 270  
 Leu

<210> 66  
 <211> 434  
 <212> PRT  
 <213> Homo sapiens

<400> 66  
 Ala Lys Gln Gln Leu Asn Leu Arg Thr His Met Ala Asp Glu Asn Lys  
 1 5 10 15  
 Asn Glu Tyr Ala Ala Gln Leu Gln Asn Phe Asn Gly Glu Gln His Lys  
 20 25 30  
 His Phe Tyr Val Val Ile Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met  
 35 40 45  
 Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala  
 50 55 60  
 Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly  
 65 70 75 80  
 Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln Met  
 85 90 95  
 Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro  
 100 105 110  
 Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly Thr  
 115 120 125  
 Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr Thr  
 130 135 140  
 Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys  
 145 150 155 160  
 Pro Gln Ser Pro Pro Leu Thr Pro Thr Ser Leu Phe Thr Ser Ser Thr



165								170				175			
Pro	Asn	Gly	Ser	Gln	Phe	Leu	Thr	Phe	Ser	Ile	Glu	Pro	Val	His	Tyr
			180					185					190		
Cys	Met	Asn	Glu	Ile	Lys	Thr	Gly	Lys	Pro	Arg	Ile	Pro	Ser	Phe	Arg
		195					200					205			
Ser	Leu	Lys	Arg	Gly	Gly	Pro	Ala	Leu	Glu	Asp	Phe	Ser	His	Leu	Pro
	210					215					220				
Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Asn
225					230					235					240
Arg	Glu	Leu	Gln	Lys	Glu	Ser	Asp	Gln	Lys	Asp	Ala	Leu	Asn	Lys	Met
				245					250					255	
Lys	Asp	Val	Tyr	Glu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Gly	Ser	Leu
			260					265					270		
Gln	Pro	Lys	Leu	Ala	Glu	Thr	Met	Asn	Asn	Ile	Asp	Arg	Leu	Arg	Met
		275					280					285			
Glu	Ile	His	Lys	Asn	Glu	Ala	Trp	Leu	Ser	Glu	Val	Glu	Gly	Lys	Thr
	290					295					300				
Gly	Gly	Arg	Gly	Asp	Arg	Arg	His	Ser	Ser	Asp	Ile	Asn	His	Leu	Val
305					310					315					320
Thr	Gln	Gly	Arg	Glu	Ser	Pro	Glu	Gly	Ser	Tyr	Thr	Asp	Asp	Ala	Asn
				325					330					335	
Gln	Glu	Val	Arg	Gly	Pro	Pro	Gln	Gln	His	Gly	His	His	Asn	Glu	Phe
			340					345					350		
Asp	Asp	Glu	Phe	Glu	Asp	Asp	Asp	Pro	Leu	Pro	Ala	Ile	Gly	His	Cys
		355					360					365			
Lys	Ala	Ile	Tyr	Pro	Phe	Asp	Gly	His	Asn	Glu	Gly	Thr	Leu	Ala	Met
	370					375					380				
Lys	Glu	Gly	Glu	Val	Leu	Tyr	Ile	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly
385					390				395						400
Trp	Thr	Arg	Ala	Arg	Arg	Gln	Asn	Gly	Glu	Glu	Gly	Tyr	Val	Pro	Thr
				405					410					415	
Ser	Tyr	Ile	Asp	Val	Thr	Leu	Glu	Lys	Asn	Ser	Lys	Gly	Ala	Val	Thr
			420					425					430		

Tyr Ile

<210> 67  
 <211> 330  
 <212> PRT

<213> Homo sapiens

<400> 67

Met	Asp	Glu	Arg	Arg	Thr	Ile	Lys	Leu	Ser	Glu	Cys	Tyr	Arg	Gly	Phe
1				5					10					15	
Ala	Asp	Ser	Glu	Arg	Lys	Val	Ile	Pro	Ile	Ile	Ser	Lys	Cys	Leu	Glu
			20					25					30		
Gly	Met	Ile	Leu	Ala	Ala	Lys	Ser	Val	Asp	Glu	Arg	Arg	Asp	Ser	Gln
		35					40					45			
Met	Val	Val	Asp	Ser	Phe	Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe
	50					55					60				
Pro	Phe	Glu	Asp	Tyr	Ser	Gln	His	Ile	Tyr	Arg	Thr	Ile	Ser	Asp	Gly
65					70					75					80
Thr	Ile	Ser	Ala	Ser	Lys	Gln	Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr
				85					90					95	
Thr	Val	Gly	Lys	Ala	Lys	Gly	Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro
			100					105					110		
Lys	Gly	Pro	Ala	Leu	Glu	Asp	Phe	Ser	His	Leu	Pro	Pro	Glu	Gln	Arg
		115					120					125			
Arg	Lys	Lys	Leu	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Asn	Arg	Glu	Leu	Gln
	130					135					140				
Lys	Glu	Ser	Asp	Gln	Lys	Asp	Ala	Leu	Asn	Lys	Met	Lys	Asp	Val	Tyr
145					150					155					160
Glu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Gly	Ser	Leu	Gln	Pro	Lys	Leu
				165					170					175	
Ala	Glu	Thr	Met	Asn	Asn	Ile	Asp	Arg	Leu	Arg	Met	Glu	Ile	His	Lys
			180					185					190		
Asn	Glu	Ala	Trp	Leu	Ser	Glu	Val	Glu	Gly	Lys	Thr	Gly	Gly	Arg	Gly
		195					200					205			
Asp	Arg	Arg	His	Ser	Ser	Asp	Ile	Asn	His	Leu	Val	Thr	Gln	Gly	Arg
	210					215					220				
Glu	Ser	Pro	Glu	Gly	Ser	Tyr	Thr	Asp	Asp	Ala	Asn	Gln	Glu	Val	Arg
225					230					235					240
Gly	Pro	Pro	Gln	Gln	His	Gly	His	His	Asn	Glu	Phe	Asp	Asp	Glu	Phe
				245					250					255	
Glu	Asp	Asp	Asp	Pro	Leu	Pro	Ala	Ile	Gly	His	Cys	Lys	Ala	Ile	Tyr
			260					265					270		
Pro	Phe	Asp	Gly	His	Asn	Glu	Gly	Thr	Leu	Ala	Met	Lys	Glu	Gly	Glu
		275					280					285			

Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ala  
 290 295 300

Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr Ser Tyr Ile Asp  
 305 310 315 320

Val Thr Leu Glu Lys Asn Ser Lys Gly Ser  
 325 330

<210> 68  
 <211> 592  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys  
 1 5 10 15

His Thr Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val  
 20 25 30

Lys Glu Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn  
 35 40 45

Leu Ser Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu  
 50 55 60

Tyr Lys Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met  
 65 70 75 80

Asn Asp Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser  
 85 90 95

Gln Ile Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu  
 100 105 110

Arg Lys Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu  
 115 120 125

Thr Cys Trp Lys Gln Leu Glu Ser Ser Lys Arg Arg Phe Glu Arg Asp  
 130 135 140

Cys Lys Glu Ala Asp Arg Ala Gln Gln Tyr Phe Glu Lys Met Asp Ala  
 145 150 155 160

Asp Ile Asn Val Thr Lys Ala Asp Val Glu Lys Ala Arg Gln Gln Ala  
 165 170 175

Gln Ile Arg His Gln Met Ala Glu Asp Ser Lys Ala Asp Tyr Ser Ser  
 180 185 190

Ile Leu Gln Lys Phe Asn His Glu Gln His Glu Tyr Tyr His Thr His  
 195 200 205

Ile Pro Asn Ile Phe Gln Lys Ile Gln Glu Met Glu Glu Arg Arg Ile  
 210 215 220

Val	Arg	Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	225	230	235	240
Val	Ile	Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	245	250	255	
Glu	Ser	Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	260	265	270	
Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	275	280	285	
Gln	Pro	Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	290	295	300	
Gly	Glu	Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	305	310	315	320
Leu	Trp	Pro	Phe	Ile	Lys	Lys	Asn	Lys	Ser	Pro	Lys	Gln	Gln	Lys	Glu	325	330	335	
Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	340	345	350	
His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	355	360	365	
Thr	Pro	Glu	Asp	Phe	Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	370	375	380	
Leu	Gln	Gln	Lys	Val	Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	385	390	395	400
Asp	Gln	Arg	Asp	Ala	Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	405	410	415	
Pro	Gln	Met	Gly	Asp	Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	420	425	430	
Ser	Gln	Asn	Ile	Glu	Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	435	440	445	
Trp	Leu	Ala	Glu	Val	Glu	Gly	Arg	Leu	Pro	Ala	Arg	Asn	Glu	Gln	Ala	450	455	460	
Arg	Arg	Gln	Ser	Gly	Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	465	470	475	480
Asn	Cys	Ala	Gln	Asp	Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	485	490	495	
Gln	Ser	Gln	Glu	Ser	Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp	500	505	510	
Glu	Phe	Asp	Asp	Glu	Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	515	520	525	

Leu Tyr Thr Phe Glu Gly Gln Asn Glu Gly Thr Ile Ser Val Val Glu  
 530 535 540  
 Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr  
 545 550 555 560  
 Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly Tyr Val Pro Thr Ser Tyr  
 565 570 575  
 Val Glu Val Cys Leu Asp Lys Asn Ala Lys Gly Ala Lys Thr Tyr Ile  
 580 585 590

<210> 69  
 <211> 679  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
 Leu Trp Asn Gly Gly Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg  
 1 5 10 15  
 Ser Cys Glu Pro Glu Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser  
 20 25 30  
 Arg Gly Ser Arg Gly Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu  
 35 40 45  
 Pro Arg Pro Pro Arg Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser  
 50 55 60  
 Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr  
 65 70 75 80  
 Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu  
 85 90 95  
 Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser  
 100 105 110  
 Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys  
 115 120 125  
 Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp  
 130 135 140  
 Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser Gln Ile  
 145 150 155 160  
 Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu Arg Lys  
 165 170 175  
 Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu Thr Cys

180						185						190					
Trp	Lys	Gln	Leu	Glu	Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys		
		195					200					205					
Glu	Ala	Asp	Arg	Ala	Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile		
	210					215					220						
Asn	Val	Thr	Lys	Ala	Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile		
225					230					235					240		
Arg	His	Gln	Met	Ala	Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu		
				245					250					255			
Gln	Lys	Phe	Asn	His	Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro		
			260					265					270				
Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg		
		275					280					285					
Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile		
	290					295					300						
Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser		
305					310					315					320		
Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser		
				325					330					335			
Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro		
			340					345					350				
Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu		
		355					360					365					
Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp		
	370					375					380						
Pro	Phe	Ile	Lys	Lys	Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His		
385					390					395					400		
Gln	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro		
				405					410					415			
Asn	Gly	Pro	Gln	Ser	Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg		
			420					425					430				
Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser		
		435					440					445					
Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	Thr	Pro	Glu	Asp	Phe		
	450					455					460						
Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val		
465					470					475					480		
Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	Asp	Gln	Arg	Asp	Ala		

485								490				495			
Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	Pro	Gln	Met	Gly	Asp
			500								505			510	
Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	Ser	Gln	Asn	Ile	Glu
			515				520						525		
Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	Trp	Leu	Ala	Glu	Val
			530				535								
Glu	Gly	Arg	Leu	Pro	Ala	Arg	Ser	Glu	Gln	Ala	Arg	Arg	Gln	Ser	Gly
545						550					555				560
Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	Asn	Cys	Ala	Gln	Asp
						565					570				575
Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	Gln	Ser	Gln	Glu	Ser
						580									590
Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp	Glu	Phe	Asp	Asp	Glu
							600						605		
Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	Leu	Tyr	Thr	Phe	Glu
							615								620
Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu	Gly	Glu	Thr	Leu	Tyr
625							630								640
Val	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	Trp	Thr	Arg	Ile	Arg	Arg	Asn
							645								655
Glu	Asp	Glu	Glu	Gly	Tyr	Val	Pro	Thr	Ser	Tyr	Val	Glu	Val	Cys	Leu
							660								670
Asp	Lys	Asn	Ala	Lys	Asp	Ser									
							675								

<210> 70  
 <211> 674  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
 Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg Ser Cys Glu Pro Glu  
 1 5 10 15  
 Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser Arg Gly Ser Arg Gly  
 20 25 30  
 Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu Pro Arg Pro Pro Arg  
 35 40 45  
 Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser Trp Gly Thr Glu Leu  
 50 55 60

Trp	Asp	Gln	Phe	Asp	Asn	Leu	Glu	Lys	His	Thr	Gln	Trp	Gly	Ile	Asp	
65					70					75					80	
Ile	Leu	Glu	Lys	Tyr	Ile	Lys	Phe	Val	Lys	Glu	Arg	Thr	Glu	Ile	Glu	
				85					90					95		
Leu	Ser	Tyr	Ala	Lys	Gln	Leu	Arg	Asn	Leu	Ser	Lys	Lys	Tyr	Gln	Pro	
			100					105					110			
Lys	Lys	Asn	Ser	Lys	Glu	Glu	Glu	Glu	Tyr	Lys	Tyr	Thr	Ser	Cys	Lys	
		115					120					125				
Ala	Phe	Ile	Ser	Asn	Leu	Asn	Glu	Met	Asn	Asp	Tyr	Ala	Gly	Gln	His	
	130					135					140					
Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser	Gln	Ile	Ile	Val	Asp	Leu	Ala	
145					150					155					160	
Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	Arg	Lys	Ser	Asn	Phe	His	Asp	
				165					170					175		
Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	Thr	Cys	Trp	Lys	Gln	Leu	Glu	
			180					185					190			
Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys	Glu	Ala	Asp	Arg	Ala	
		195					200					205				
Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile	Asn	Val	Thr	Lys	Ala	
	210					215					220					
Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile	Arg	His	Gln	Met	Ala	
225					230					235					240	
Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu	Gln	Lys	Phe	Asn	His	
				245					250					255		
Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro	Asn	Ile	Phe	Gln	Lys	
			260					265					270			
Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg	Met	Gly	Glu	Ser	Met	
		275					280					285				
Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile	Pro	Ile	Ile	Gly	Lys	
	290					295					300					
Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser	Ile	Asp	Gln	Lys	Asn	
305					310					315					320	
Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser	Gly	Phe	Glu	Pro	Pro	
				325					330					335		
Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro	Met	Lys	Arg	Thr	Val	
			340					345					350			
Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu	Gly	Lys	Pro	Asp	Leu	
		355					360					365				



Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp	Pro	Phe	Ile	Lys	Lys	370	375	380	
Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His	Gln	Pro	Pro	Pro	Pro	385	390	395	400
Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro	Asn	Gly	Pro	Gln	Ser	405	410	415	
Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met	420	425	430	
Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu	435	440	445	
Ser	Leu	Lys	Leu	Gly	Ala	Thr	Pro	Glu	Asp	Phe	Ser	Asn	Leu	Pro	Pro	450	455	460	
Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val	Asp	Glu	Leu	Asn	Lys	465	470	475	480
Glu	Ile	Gln	Lys	Glu	Met	Asp	Gln	Arg	Asp	Ala	Ile	Thr	Lys	Met	Lys	485	490	495	
Asp	Val	Tyr	Leu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Ala	Ser	Leu	Asp	500	505	510	
His	Lys	Leu	Ala	Glu	Val	Ser	Gln	Asn	Ile	Glu	Lys	Leu	Arg	Val	Glu	515	520	525	
Thr	Gln	Lys	Phe	Glu	Ala	Trp	Leu	Ala	Glu	Val	Glu	Gly	Arg	Leu	Pro	530	535	540	
Ala	Arg	Ser	Glu	Gln	Ala	Arg	Arg	Gln	Ser	Gly	Leu	Tyr	Asp	Ser	Gln	545	550	555	560
Asn	Pro	Pro	Thr	Val	Asn	Asn	Cys	Ala	Gln	Asp	Arg	Glu	Ser	Pro	Asp	565	570	575	
Gly	Ser	Tyr	Thr	Glu	Glu	Gln	Ser	Gln	Glu	Ser	Glu	Met	Lys	Val	Leu	580	585	590	
Ala	Thr	Asp	Phe	Asp	Asp	Glu	Phe	Asp	Asp	Glu	Glu	Pro	Leu	Pro	Ala	595	600	605	
Ile	Gly	Thr	Cys	Lys	Ala	Leu	Tyr	Thr	Phe	Glu	Gly	Gln	Asn	Glu	Gly	610	615	620	
Thr	Ile	Ser	Val	Val	Glu	Gly	Glu	Thr	Leu	Tyr	Val	Ile	Glu	Glu	Asp	625	630	635	640
Lys	Gly	Asp	Gly	Trp	Thr	Arg	Ile	Arg	Arg	Asn	Glu	Asp	Glu	Glu	Gly	645	650	655	
Tyr	Val	Pro	Thr	Ser	Tyr	Val	Glu	Val	Cys	Leu	Asp	Lys	Asn	Ala	Lys	660	665	670	

Asp Ser

<210> 71

<211> 457

<212> PRT

<213> Homo sapiens

<400> 71

Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala  
1 5 10 15

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln  
20 25 30

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly  
35 40 45

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly  
50 55 60

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile  
65 70 75 80

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala  
85 90 95

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe  
100 105 110

Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln  
115 120 125

Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly  
130 135 140

Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys  
145 150 155 160

Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala  
165 170 175

Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro  
180 185 190

Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu  
195 200 205

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val  
210 215 220

Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg  
225 230 235 240

His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala  
245 250 255

Ala	His	Cys	Met	His	Ser	Phe	Arg	Leu	Ala	Arg	Leu	Ser	Ser	Trp	Arg		
			260					265					270				
Val	His	Ala	Gly	Leu	Val	Ser	His	Ser	Ala	Val	Arg	Pro	His	Gln	Gly		
		275					280					285					
Ala	Leu	Val	Glu	Arg	Ile	Ile	Pro	His	Pro	Leu	Tyr	Ser	Ala	Gln	Asn		
	290					295					300						
His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Arg	Leu	Gln	Thr	Ala	Leu	Asn	Phe		
305					310					315					320		
Ser	Asp	Thr	Val	Gly	Ala	Val	Cys	Leu	Pro	Ala	Lys	Glu	Gln	His	Phe		
				325					330					335			
Pro	Lys	Gly	Ser	Arg	Cys	Trp	Val	Ser	Gly	Trp	Gly	His	Thr	His	Pro		
			340					345					350				
Ser	His	Thr	Tyr	Ser	Ser	Asp	Met	Leu	Gln	Asp	Thr	Val	Val	Pro	Leu		
		355					360					365					
Phe	Ser	Thr	Gln	Leu	Cys	Asn	Ser	Ser	Cys	Val	Tyr	Ser	Gly	Ala	Leu		
	370					375					380						
Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Asp	Gly	Arg	Ala	Asp	Ala		
385					390					395					400		
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Pro	Asp	Gly	Asp	Thr		
				405					410					415			
Trp	Arg	Leu	Val	Gly	Val	Val	Ser	Trp	Gly	Arg	Ala	Cys	Ala	Glu	Pro		
			420					425					430				
Asn	His	Pro	Gly	Val	Tyr	Ala	Lys	Val	Ala	Glu	Phe	Leu	Asp	Trp	Ile		
		435					440					445					
His	Asp	Thr	Ala	Gln	Asp	Ser	Leu	Leu									
	450					455											

<210> 72  
 <211> 455  
 <212> PRT  
 <213> Mus musculus

<400> 72  
 Met Ser Pro Thr Leu Asp Asp Gln Ser Pro Met Glu Ile Arg Cys Thr  
 1 5 10 15  
 Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg Met Glu Leu Gly Asp Gln  
 20 25 30  
 Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp Cys Cys Leu Gln Arg Gly  
 35 40 45  
 Cys Val Ile Leu Gly Val Leu Gly Leu Leu Ala Gly Ala Gly Ile Ala

50					55					60					
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Trp	Pro	Ala	Ala	Ser	Pro	Ser	Ile
65					70					75					80
Ser	Gly	Thr	Leu	Gln	Glu	Glu	Glu	Met	Thr	Leu	Asn	Cys	Pro	Gly	Val
				85					90					95	
Ser	Cys	Glu	Glu	Glu	Leu	Leu	Pro	Ser	Leu	Pro	Lys	Thr	Val	Ser	Phe
			100					105					110		
Arg	Ile	Asn	Gly	Glu	Asp	Leu	Leu	Leu	Gln	Val	Gln	Val	Arg	Ala	Arg
		115					120					125			
Pro	Asp	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly
		130				135					140				
Met	His	Ile	Cys	Lys	Ser	Leu	Gly	His	Ile	Arg	Leu	Thr	Gln	His	Lys
145					150					155					160
Ala	Val	Asn	Leu	Ser	Asp	Ile	Lys	Leu	Asn	Arg	Ser	Gln	Glu	Phe	Ala
				165					170					175	
Gln	Leu	Ser	Ala	Arg	Pro	Gly	Gly	Leu	Val	Glu	Glu	Ala	Trp	Lys	Pro
			180					185					190		
Ser	Ala	Asn	Cys	Pro	Ser	Gly	Arg	Ile	Val	Ser	Leu	Lys	Cys	Ser	Glu
		195					200					205			
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ala	Val
	210					215					220				
Ala	Ser	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Met	Leu	Gly	Ser	Arg
225					230					235					240
His	Thr	Cys	Gly	Ala	Ser	Val	Leu	Ala	Pro	His	Trp	Val	Val	Thr	Ala
				245					250					255	
Ala	His	Cys	Met	Tyr	Ser	Phe	Arg	Leu	Ser	Arg	Leu	Ser	Ser	Trp	Arg
			260					265					270		
Val	His	Ala	Gly	Leu	Val	Ser	His	Gly	Ala	Val	Arg	Gln	His	Gln	Gly
		275					280					285			
Thr	Met	Val	Glu	Lys	Ile	Ile	Pro	His	Pro	Leu	Tyr	Ser	Ala	Gln	Asn
	290					295					300				
His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu	Arg	Thr	Pro	Ile	Asn	Phe
305					310					315					320
Ser	Asp	Thr	Val	Asp	Ala	Val	Cys	Leu	Pro	Ala	Lys	Glu	Gln	Tyr	Phe
				325					330					335	
Pro	Trp	Gly	Ser	Gln	Cys	Trp	Val	Ser	Gly	Trp	Gly	His	Thr	Asp	Pro
			340					345					350		
Ser	His	Thr	His	Ser	Ser	Asp	Thr	Leu	Gln	Asp	Thr	Met	Val	Pro	Leu

355	360	365
Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu		
370	375	380
Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala		
385	390	395
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr		
	405	410
Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro		
	420	425
Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile		
	435	440
His Asp Thr Val Gln Val Arg		
450	455	

<210> 73  
 <211> 445  
 <212> PRT  
 <213> Mus musculus

<400> 73

Met Glu Ile Arg Cys Thr Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg
1 5 10 15
Met Glu Leu Gly Asp Gln Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp
20 25 30
Cys Cys Leu Gln Arg Gly Cys Val Ile Leu Gly Val Leu Gly Leu Leu
35 40 45
Ala Gly Ala Gly Ile Ala Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro
50 55 60
Ala Ala Ser Pro Ser Ile Ser Gly Thr Leu Gln Glu Glu Glu Met Thr
65 70 75 80
Leu Asn Cys Pro Gly Val Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu
85 90 95
Pro Lys Thr Val Ser Phe Arg Ile Asn Gly Glu Asp Leu Leu Leu Gln
100 105 110
Val Gln Val Arg Ala Arg Pro Asp Trp Leu Leu Val Cys His Glu Gly
115 120 125
Trp Ser Pro Ala Leu Gly Met His Ile Cys Lys Ser Leu Gly His Ile
130 135 140
Arg Leu Thr Gln His Lys Ala Val Asn Leu Ser Asp Ile Lys Leu Asn
145 150 155 160

Arg	Ser	Gln	Glu	Phe	Ala	Gln	Leu	Ser	Ala	Arg	Pro	Gly	Gly	Leu	Val			
				165					170					175				
Glu	Glu	Ala	Trp	Lys	Pro	Ser	Ala	Asn	Cys	Pro	Ser	Gly	Arg	Ile	Val			
			180					185					190					
Ser	Leu	Lys	Cys	Ser	Glu	Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile			
		195					200					205						
Val	Gly	Gly	Gln	Ala	Val	Ala	Ser	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser			
	210					215					220							
Val	Met	Leu	Gly	Ser	Arg	His	Thr	Cys	Gly	Ala	Ser	Val	Leu	Ala	Pro			
225					230					235					240			
His	Trp	Val	Val	Thr	Ala	Ala	His	Cys	Met	Tyr	Ser	Phe	Arg	Leu	Ser			
				245					250					255				
Arg	Leu	Ser	Ser	Trp	Arg	Val	His	Ala	Gly	Leu	Val	Ser	His	Gly	Ala			
			260					265					270					
Val	Arg	Gln	His	Gln	Gly	Thr	Met	Val	Glu	Lys	Ile	Ile	Pro	His	Pro			
		275					280					285						
Leu	Tyr	Ser	Ala	Gln	Asn	His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu			
	290					295					300							
Arg	Thr	Pro	Ile	Asn	Phe	Ser	Asp	Thr	Val	Gly	Ala	Val	Cys	Leu	Pro			
305					310					315					320			
Ala	Lys	Glu	Gln	Tyr	Phe	Pro	Trp	Gly	Ser	Gln	Cys	Trp	Val	Ser	Gly			
				325					330					335				
Trp	Gly	His	Thr	Asp	Pro	Ser	His	Thr	His	Ser	Ser	Asp	Thr	Leu	Gln			
			340					345					350					
Asp	Thr	Met	Val	Pro	Leu	Leu	Ser	Thr	His	Leu	Cys	Asn	Ser	Ser	Cys			
		355					360					365						
Met	Tyr	Ser	Gly	Ala	Leu	Thr	His	Arg	Met	Leu	Cys	Ala	Gly	Tyr	Leu			
	370					375					380							
Asp	Gly	Arg	Ala	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val			
385					390					395					400			
Cys	Pro	Ser	Gly	Asp	Thr	Trp	His	Leu	Val	Gly	Val	Val	Ser	Trp	Gly			
				405					410					415				
Arg	Gly	Cys	Ala	Glu	Pro	Asn	Arg	Pro	Gly	Val	Tyr	Ala	Lys	Val	Ala			
			420					425					430					
Glu	Phe	Leu	Asp	Trp	Ile	His	Asp	Thr	Val	Gln	Val	Arg						
		435					440					445						

<210> 74  
<211> 398

<212> PRT

<213> Homo sapiens

<400> 74

Met	Ser	Leu	Met	Leu	Asp	Asp	Gln	Pro	Pro	Met	Glu	Ala	Gln	Tyr	Ala	
1				5					10						15	
Glu	Glu	Gly	Pro	Gly	Pro	Gly	Ile	Phe	Arg	Ala	Glu	Pro	Gly	Asp	Gln	
			20					25					30			
Gln	His	Pro	Ile	Ser	Gln	Ala	Val	Cys	Trp	Arg	Ser	Met	Arg	Arg	Gly	
		35					40					45				
Cys	Ala	Val	Leu	Gly	Ala	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Val	Gly	
	50					55					60					
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Cys	Pro	Ala	Ala	Ser	Gln	Pro	Ile	
65					70					75					80	
Ser	Gly	Thr	Leu	Gln	Asp	Glu	Glu	Ile	Thr	Leu	Ser	Cys	Ser	Glu	Ala	
				85					90						95	
Ser	Ala	Glu	Glu	Ala	Leu	Leu	Pro	Ala	Leu	Pro	Lys	Thr	Val	Ser	Phe	
			100					105					110			
Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln	
		115					120					125				
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly	
	130					135					140					
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys	
145					150					155					160	
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala	
				165					170					175		
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro	
			180					185					190			
Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val	Val	Ser	Leu	Arg	Cys	Ser	Glu	
		195					200					205				
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ser	Val	
	210					215					220					
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg	
225					230					235					240	
His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala	
				245					250					255		
Ala	His	Cys	Met	His	Ser	Phe	Arg	Leu	Ala	Arg	Leu	Ser	Ser	Trp	Arg	
			260					265					270			
Val	His	Ala	Gly	Leu	Val	Ser	His	Ser	Ala	Val	Arg	Pro	His	Gln	Gly	
		275					280					285				

Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn  
290 295 300

His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe  
305 310 315 320

Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe  
325 330 335

Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro  
340 345 350

Ser His Ser Leu Gln Leu Gly Tyr Ala Pro Gly His Gly Gly Ala Leu  
355 360 365

Val Gln His Ser Ala Leu Gln Gln Leu Leu Arg Val Gln Arg Ser Pro  
370 375 380

His Pro Pro His Ala Leu Arg Trp Leu Pro Gly Arg Lys Gly  
385 390 395

<210> 75  
<211> 311  
<212> PRT  
<213> Mus musculus

<400> 75  
Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys  
1 5 10 15

Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala  
20 25 30

Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro  
35 40 45

Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu  
50 55 60

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val  
65 70 75 80

Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg  
85 90 95

His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala  
100 105 110

Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg  
115 120 125

Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly  
130 135 140

Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn



145		150		155		160
His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe						
	165			170		175
Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe						
	180		185			190
Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro						
	195		200			205
Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu						
	210		215			220
Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu						
	225		230		235	240
Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala						
		245		250		255
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr						
	260		265			270
Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro						
	275		280			285
Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile						
	290		295			300
His Asp Thr Val Gln Val Arg						
	305		310			

<210> 76  
 <211> 199  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Reprolysin  
 family zinc protease Consensus Sequence

<400> 76
Lys Tyr Ile Glu Leu Phe Ile Val Val Asp His Gly Met Phe Thr Lys
1 5 10 15
Tyr Gly Ser Asp Leu Asn Lys Ile Arg Gln Arg Val His Gln Ile Val
20 25 30
Asn Leu Val Asn Glu Ile Tyr Arg Pro Leu Asn Ile Arg Val Val Leu
35 40 45
Val Gly Leu Glu Ile Trp Ser Asp Gly Asp Lys Ile Thr Val Gln Gly
50 55 60
Asp Ala Asn Asp Thr Leu His Arg Phe Leu Glu Trp Arg Glu Thr Asp
65 70 75 80

Leu Leu Lys Arg Lys Ser His Asp Asn Ala Gln Leu Leu Thr Gly Ile  
                     85                    90                    95  
 Asp Phe Asp Gly Asn Thr Ile Gly Ala Ala Tyr Val Gly Gly Met Cys  
                     100                    105                    110  
 Ser Pro Lys Arg Ser Val Gly Val Val Gln Asp His Ser Pro Ile Val  
                     115                    120                    125  
 Leu Leu Val Ala Val Thr Met Ala His Glu Leu Gly His Asn Leu Gly  
                     130                    135                    140  
 Met Thr His Asp Asp Ile Asn Lys Cys Thr Cys Glu Gly Gly Gly Gly  
 145                    150                    155                    160  
 Cys Ile Met Asn Pro Val Ala Ser Ser Ser Pro Gly Lys Lys Phe Ser  
                     165                    170                    175  
 Asn Cys Ser Met Asp Asp Tyr Gln Gln Phe Leu Thr Lys Gly Lys Pro  
                     180                    185                    190  
 Gln Cys Leu Leu Asn Lys Pro  
                     195

<210> 77  
 <211> 51  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Thrombospondin  
           type 1 Consensus Sequence

<400> 77  
 Trp Gly Glu Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Gly  
   1                    5                    10                    15  
 Gly Val Gln Thr Arg Thr Arg Cys Cys Asn Pro Pro Pro Asn Gly Gly  
                     20                    25                    30  
 Gly Pro Cys Thr Gly Pro Asp Thr Glu Thr Arg Ala Cys Asn Glu Gln  
                     35                    40                    45  
 Pro Cys Pro  
           50

<210> 78  
 <211> 48  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Thrombospondin  
           type 1 domain Consensus Sequence

<400> 78

Ser Pro Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Lys Gly  
1 5 10 15

Ile Arg Thr Arg Gln Arg Thr Cys Asn Ser Pro Ala Gly Gly Lys Pro  
20 25 30

Cys Thr Gly Asp Ala Gln Glu Thr Glu Ala Cys Met Met Asp Pro Cys  
35 40 45

<210> 79

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reprolysin  
family propeptide Consensus Sequence

<400> 79

His Leu Glu Lys Asn Arg Ser Leu Leu Ala Pro Asp Phe Thr Val Thr  
1 5 10 15

Thr Tyr Asp Asp Asp Gly Thr Leu Val Thr Glu His Pro Leu Ile Gln  
20 25 30

Asp His Cys Tyr Tyr Gln Gly Tyr Val Glu Gly Tyr Pro Asn Ser Ala  
35 40 45

Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Leu Glu  
50 55 60

Asn Leu Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ser Asp Gly Phe Glu  
65 70 75 80

His Ile Ile Tyr Gln Ile Glu His Leu Lys Thr Val Pro Gly Pro Cys  
85 90 95

Gly Glu Cys Gly Ser Leu Ser Val Ser Thr Asp Ser Gln Tyr Gly Ile  
100 105 110

Arg Ser Pro Ser Pro  
115

<210> 80

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

# Alpha-2-macroglobulin family Consensus Sequence

<400> 80

Ile Asp Glu Asp Asp Ile Thr Ile Arg Ser Tyr Phe Pro Glu Ser Trp  
1 5 10 15

Leu Trp Glu Val Glu Glu Val Asp Arg Ser Pro Val Leu Thr Val Asn  
20 25 30

Ile Thr Leu Pro Asp Ser Ile Thr Thr Trp Glu Ile Leu Ala Val Ser  
35 40 45

Leu Ser Asn Thr Lys Gly Leu Cys Val Ala Asp Pro Val Glu Leu Thr  
50 55 60

Val Phe Gln Asp Phe Phe Leu Glu Leu Arg Leu Pro Tyr Ser Val Val  
65 70 75 80

Arg Gly Glu Gln Val Glu Leu Arg Ala Val Leu Tyr Asn Tyr Leu Pro  
85 90 95

Ser Gln Asp Ile Lys Val Val Val Gln Leu Glu Val Glu Pro Leu Cys  
100 105 110

Gln Ala Gly Phe Cys Ser Leu Ala Thr Gln Arg Thr Arg Ser Ser Gln  
115 120 125

Ser Val Arg Pro Lys Ser Leu Ser Ser Val Ser Phe Pro Val Val Val  
130 135 140

Val Pro Leu Ala Ser Gly Leu Ser Leu Val Glu Val Val Ala Ser Val  
145 150 155 160

Pro Glu Phe Phe Val Lys Asp Ala Val Val Lys Thr Leu Lys Val Glu  
165 170 175

Pro Glu Gly Ala Arg Lys Glu Glu Thr Val Ser Ser Leu Leu Leu Pro  
180 185 190

Pro Glu His Leu Gly Gly Gly Leu Glu Val Ser Glu Val Pro Ala Leu  
195 200 205

Lys Leu Pro Asp Asp Val Pro Asp Thr Glu Ala Glu Ala Val Ile Ser  
210 215 220

Val Gln Gly Asp Pro Val Ala Gln Ala Ile Gln Asn Thr Leu Ser Gly  
225 230 235 240

Glu Gly Leu Asn Asn Leu Leu Arg Leu Pro Ser Gly Cys Gly Glu Gln  
245 250 255

Asn Met Ile Tyr Met Ala Pro Thr Val Tyr Val Leu His Tyr Leu Asp  
260 265 270

Glu Thr Trp Gln Trp Glu Lys Pro Gly Thr Lys Lys Lys Gln Lys Ala  
275 280 285

Ile	Asp	Leu	Ile	Asn	Lys	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Arg	Lys	290	295	300			
Ala	Asp	Gly	Ser	Tyr	Ala	Ala	Phe	Leu	His	Arg	Ala	Ser	Ser	Thr	Trp	305	310	315	320		
Leu	Thr	Ala	Phe	Val	Leu	Lys	Val	Phe	Ser	Gln	Ala	Arg	Asn	Tyr	Val		325	330	335		
Phe	Ile	Asp	Glu	Glu	His	Ile	Cys	Gly	Ala	Val	Lys	Trp	Leu	Ile	Leu		340	345	350		
Asn	Gln	Gln	Lys	Asp	Asp	Gly	Val	Phe	Arg	Glu	Ser	Gly	Pro	Val	Ile		355	360	365		
His	Asn	Glu	Met	Lys	Gly	Gly	Val	Gly	Asp	Asp	Ala	Glu	Val	Glu	Val		370	375	380		
Thr	Leu	Thr	Ala	Phe	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ala	Lys	Leu	Val		385	390	395	400	
Cys	Ile	Ser	Pro	Val	Val	Ala	Asn	Ala	Leu	Ser	Ile	Leu	Lys	Ala	Ser		405	410		415	
Asp	Tyr	Leu	Leu	Glu	Asn	Tyr	Ala	Asn	Gly	Gln	Arg	Val	Tyr	Thr	Leu		420	425		430	
Ala	Leu	Thr	Ala	Tyr	Ala	Leu	Ala	Leu	Ala	Gly	Val	Leu	His	Lys	Leu		435	440		445	
Lys	Glu	Ile	Leu	Lys	Ser	Leu	Lys	Glu	Glu	Leu	Tyr	Lys	Ala	Leu	Val		450	455		460	
Lys	Gly	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Asp	Ala	Pro	Gly	His		465	470		475	480
Pro	Tyr	Ser	Pro	Gln	Pro	Gln	Ala	Ala	Ala	Val	Glu	Met	Thr	Ser	Tyr		485	490		495	
Ala	Leu	Leu	Ala	Leu	Leu	Thr	Leu	Leu	Pro	Phe	Pro	Lys	Val	Glu	Met		500	505		510	
Ala	Pro	Lys	Val	Val	Lys	Trp	Leu	Thr	Glu	Gln	Gln	Tyr	Tyr	Gly	Gly		515	520		525	
Gly	Phe	Gly	Ser	Thr	Gln	Asp	Thr	Val	Met	Ala	Leu	Gln	Ala	Leu	Ser		530	535		540	
Lys	Tyr	Gly	Ile	Ala	Thr	Pro	Thr	His	Lys	Glu	Lys	Asn	Leu	Ser	Val		545	550		555	560
Thr	Ile	Gln	Ser	Pro	Ser	Gly	Ser	Phe	Lys	Ser	His	Phe	Gln	Ile	Leu		565	570		575	
Asn	Asn	Asn	Ala	Phe	Leu	Leu	Arg	Pro	Val	Glu	Leu	Pro	Leu	Asn	Glu		580	585		590	

Gly Phe Thr Val Thr Ala Lys Val Thr Gly Gln Gly Thr Leu Thr Leu  
 595 600 605  
 Val Thr Thr Tyr Arg Tyr Lys Val Leu Asp Lys Lys Asn Thr Phe Cys  
 610 615 620  
 Phe Asp Leu Lys Ile Glu Thr Val Pro Asp Thr Cys Val Glu Pro Lys  
 625 630 635 640  
 Gly Ala Lys Asn Ser Asp Tyr Leu Ser Ile Cys Thr Arg Tyr Ala Gly  
 645 650 655  
 Ser Arg Ser Asp Ser Gly Met Ala Ile Ala Asp Ile Ser Met Leu Thr  
 660 665 670  
 Gly Phe Ile Pro Leu Lys Pro Asp Leu Lys Lys Leu Glu Asn Gly Val  
 675 680 685  
 Asp Arg Tyr Val Ser Lys Tyr Glu Ile Asp Gly Asn His Val Leu Leu  
 690 695 700  
 Tyr Leu Asp Lys Val Ser His Ser Glu Thr Glu Cys Val Gly Phe Lys  
 705 710 715 720  
 Ile His Gln Asp Phe Glu Val Gly Leu Leu Gln Pro Ala Ser Val Lys  
 725 730 735  
 Val Tyr Asp Tyr Tyr Glu Pro Asp Glu Gln Cys Thr Ala Phe Tyr  
 740 745 750

<210> 81  
 <211> 620  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 Alpha-2-macroglobulin family N-terminal region  
 Consensus Sequence

<400> 81  
 Arg Leu Leu Trp Leu Leu Leu Leu Leu Leu Phe Phe Asp Ser Ser  
 1 5 10 15  
 Leu Gln Lys Pro Arg Tyr Met Val Ile Val Pro Ser Ile Leu Arg Thr  
 20 25 30  
 Glu Thr Pro Glu Lys Val Cys Val Gln Leu His Asp Leu Asn Glu Thr  
 35 40 45  
 Val Thr Val Thr Val Ser Leu His Ser Phe Pro Gly Lys Arg Asn Leu  
 50 55 60  
 Ser Ser Leu Phe Thr Val Leu Leu Ser Ser Lys Asp Leu Phe His Cys  
 65 70 75 80

Val	Ser	Phe	Thr	Val	Pro	Gln	Pro	Gly	Leu	Phe	Lys	Ser	Ser	Lys	Gly	85	90	95
Glu	Glu	Ser	Phe	Val	Val	Val	Gln	Val	Lys	Gly	Pro	Thr	His	Thr	Phe	100	105	110
Lys	Glu	Lys	Val	Thr	Val	Leu	Val	Ser	Ser	Arg	Arg	Gly	Leu	Val	Phe	115	120	125
Ile	Gln	Thr	Asp	Lys	Pro	Ile	Tyr	Thr	Pro	Gly	Gln	Thr	Val	Arg	Tyr	130	135	140
Arg	Val	Phe	Ser	Val	Asp	Glu	Asn	Leu	Arg	Pro	Leu	Asn	Glu	Leu	Ile	145	150	155
Leu	Val	Tyr	Ile	Glu	Asp	Pro	Glu	Gly	Asn	Arg	Val	Asp	Gln	Trp	Glu	165	170	175
Val	Asn	Lys	Leu	Glu	Gly	Gly	Ile	Phe	Gln	Leu	Ser	Phe	Pro	Ile	Pro	180	185	190
Ser	Glu	Pro	Ile	Gln	Gly	Thr	Trp	Lys	Ile	Val	Ala	Arg	Tyr	Glu	Ser	195	200	205
Gly	Pro	Glu	Ser	Asn	Tyr	Thr	His	Tyr	Phe	Glu	Val	Lys	Glu	Tyr	Val	210	215	220
Leu	Pro	Ser	Phe	Glu	Val	Ser	Ile	Thr	Pro	Pro	Lys	Pro	Phe	Ile	Tyr	225	230	235
Tyr	Asp	Asn	Phe	Lys	Glu	Phe	Glu	Val	Thr	Ile	Cys	Ala	Arg	Tyr	Thr	245	250	255
Tyr	Gly	Lys	Pro	Val	Pro	Gly	Val	Ala	Tyr	Val	Arg	Phe	Gly	Val	Lys	260	265	270
Asp	Glu	Asp	Gly	Lys	Lys	Glu	Leu	Leu	Ala	Gly	Leu	Glu	Glu	Arg	Ala	275	280	285
Lys	Leu	Leu	Asp	Gly	Asn	Gly	Glu	Ile	Cys	Leu	Ser	Gln	Glu	Val	Leu	290	295	300
Leu	Lys	Glu	Leu	Gln	Leu	Lys	Asn	Glu	Asp	Leu	Glu	Gly	Lys	Ser	Leu	305	310	315
Tyr	Val	Ala	Val	Ala	Val	Ile	Glu	Ser	Glu	Gly	Gly	Asp	Met	Glu	Glu	325	330	335
Ala	Glu	Leu	Gly	Gly	Ile	Lys	Ile	Val	Arg	Ser	Pro	Tyr	Lys	Leu	Lys	340	345	350
Phe	Val	Lys	Thr	Pro	Ser	His	Phe	Lys	Pro	Gly	Ile	Pro	Phe	Phe	Leu	355	360	365
Lys	Val	Leu	Val	Val	Asp	Pro	Asp	Gly	Ser	Pro	Ala	Pro	Asn	Val	Pro	370	375	380

Val Lys Val Ser Ala Gln Asp Ala Ser Tyr Tyr Ser Asn Gly Thr Thr  
 385 390 395 400  
 Asp Glu Asp Gly Leu Ala Gln Phe Ser Ile Asn Thr Ser Gly Ile Ser  
 405 410 415  
 Ser Leu Ser Ile Thr Val Arg Thr Asn His Lys Glu Leu Pro Glu Glu  
 420 425 430  
 Val Gln Ala His Ala Glu Ala Gln Ala Thr Ala Tyr Ser Thr Val Ser  
 435 440 445  
 Leu Ser Lys Ser Tyr Ile His Leu Ser Ile Glu Arg Thr Leu Pro Cys  
 450 455 460  
 Gly Pro Gly Val Gly Glu Gln Ala Asn Phe Ile Leu Arg Gly Lys Ser  
 465 470 475 480  
 Leu Gly Glu Leu Lys Ile Leu His Phe Tyr Tyr Leu Ile Met Ser Lys  
 485 490 495  
 Gly Lys Ile Val Lys Thr Gly Arg Glu Pro Arg Glu Pro Gly Gln Gly  
 500 505 510  
 Leu Phe Ser Leu Ser Ile Pro Val Thr Pro Asp Leu Ala Pro Ser Phe  
 515 520 525  
 Arg Leu Val Ala Tyr Tyr Ile Leu Pro Gln Gly Glu Val Val Ala Asp  
 530 535 540  
 Ser Val Trp Ile Asp Val Glu Asp Cys Cys Ala Asn Lys Leu Asp Leu  
 545 550 555 560  
 Ser Phe Ser Pro Ser Lys Asp Tyr Arg Leu Pro Ala Gln Gln Val Lys  
 565 570 575  
 Leu Arg Val Glu Ala Asp Pro Gln Ser Leu Val Ala Leu Arg Ala Val  
 580 585 590  
 Asp Gln Ala Val Tyr Leu Leu Lys Pro Lys Ala Lys Leu Ser Met Ser  
 595 600 605  
 Lys Val Tyr Asp Leu Leu Glu Lys Ser Asp Leu Gly  
 610 615 620

<210> 82

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sodium Bile  
acid symporter family consensus sequence

<400> 82

Ala Leu Gly Leu Phe Leu Met Met Phe Ser Met Gly Leu Lys Val Arg



1	5	10	15
Phe Glu Asp Leu Lys Glu Ala Leu Arg Arg Pro Lys Ala Leu Ile Leu	20	25	30
Gly Leu Leu Leu Gln Trp Ile Ile Met Pro Leu Leu Met Phe Ile Leu	35	40	45
Ala Trp Leu Leu Leu Arg Leu Pro Pro Glu Leu Ala Thr Gly Leu Ile	50	55	60
Leu Val Gly Cys Ala Pro Gly Gly Ala Met Ser Asn Val Trp Thr Tyr	65	70	75
Leu Ala Lys Gly Asp Val Glu Leu Ser Val Val Met Val Ala Leu Ser	85	90	95
Thr Leu Leu Ala Pro Leu Val Thr Pro Leu Leu Ser Phe Leu Leu Ala	100	105	110
Gly Leu Leu Val His Val Asp Ala Val Ser Pro Trp Ser Leu Ile Lys	115	120	125
Ser Val Leu Val Tyr Val Ile Ile Pro Leu Ile Ala Gly Met Leu Thr	130	135	140
Arg Tyr Phe Leu Pro Glu Trp Phe Glu Gln Arg Val Leu Pro Val Leu	145	150	155
Ser Pro Ile Ser Leu Ile Gly Leu Leu Leu Thr Ile Val Val Ile Phe	165	170	175
Ala Leu Asn Gly Glu Val Ile Ala Ser Leu	180	185	

<210> 83

<211> 191

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SPFH  
domain/Band 7 family Consensus Sequence

<400> 83

Val Ala Leu Leu Ile Ile Ile Ala Leu Val Val Ile Ala Met Ser Val	1	5	10	15
Lys Ile Val Lys Glu Tyr Glu Arg Gly Val Ile Phe Arg Leu Gly Arg	20	25	30	
Tyr Val Arg Gln Val Val Gly Pro Gly Leu His Phe Ile Ile Pro Phe	35	40	45	
Ile Asp Thr Val Lys Lys Val Asp Leu Arg Thr Val Val Tyr Asp Val	50	55	60	

Pro Ser Gln Glu Ile Ile Thr Lys Asp Asn Val Val Val Ile Val Asp  
 65 70 75 80  
 Ala Val Val Tyr Tyr Arg Val Val Asp Pro Leu Lys Ala Val Tyr Glu  
 85 90 95  
 Val Glu Asp Ala Glu Arg Ala Leu Pro Gln Leu Ala Gln Thr Thr Leu  
 100 105 110  
 Arg Asn Val Ile Gly Gln Phe Thr Leu Asp Glu Ile Leu Thr Glu Arg  
 115 120 125  
 Glu Arg Ile Asn Ser Gln Leu Arg Glu Ile Leu Asp Glu Ala Thr Asp  
 130 135 140  
 Pro Trp Gly Ile Lys Val Glu Arg Val Glu Ile Lys Asp Ile Arg Leu  
 145 150 155 160  
 Pro Glu Glu Val Gln Arg Ala Met Ala Ala Gln Met Glu Ala Glu Arg  
 165 170 175  
 Glu Ala Arg Ala Lys Ile Leu Glu Ala Glu Gly Glu Gln Glu Ala  
 180 185 190

<210> 84  
 <211> 160  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Prohibitin  
 homologues Consensus Sequence

<400> 84  
 Ala Ala Phe Tyr Val Ile Gly Glu Gly Glu Arg Gly Val Val Glu Arg  
 1 5 10 15  
 Leu Gly Arg Val Leu Lys Val Leu Gly Pro Gly Leu His Phe Val Ile  
 20 25 30  
 Pro Phe Ile Asp Asp Val Lys Arg Val Asp Leu Arg Ala Gln Thr Asp  
 35 40 45  
 Asp Val Pro Pro Gln Glu Val Ile Thr Lys Asp Asn Val Thr Val Ser  
 50 55 60  
 Val Asp Ala Val Val Tyr Tyr Arg Val Leu Asp Pro Leu Lys Ala Val  
 65 70 75 80  
 Tyr Gly Val Leu Asp Ala Asp Tyr Arg Ala Leu Arg Gln Leu Ala Gln  
 85 90 95  
 Thr Thr Leu Arg Ser Val Ile Gly Lys Arg Thr Leu Asp Glu Leu Leu  
 100 105 110

Thr Asp Glu Arg Glu Lys Ile Ser Glu Asn Ile Arg Glu Glu Leu Asn  
115 120 125

Glu Ala Ala Glu Pro Trp Gly Ile Glu Val Glu Asp Val Glu Ile Lys  
130 135 140

Asp Ile Arg Leu Pro Glu Glu Ile Lys Glu Ala Met Glu Ala Gln Gln  
145 150 155 160

<210> 85  
<211> 79  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Kringle domain  
Consensus Sequence

<400> 85  
Cys Tyr His Gly Asn Gly Glu Asn Tyr Arg Gly Thr Ala Ser Thr Thr  
1 5 10 15

Glu Ser Gly Ala Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro His Arg  
20 25 30

His Ser Lys Tyr Thr Pro Glu Arg Tyr Pro Ala Lys Gly Leu Gly Glu  
35 40 45

Asn Tyr Cys Arg Asn Pro Asp Gly Asp Glu Arg Pro Trp Cys Tyr Thr  
50 55 60

Thr Asp Pro Arg Val Arg Trp Glu Tyr Cys Asp Ile Pro Arg Cys  
65 70 75

<210> 86  
<211> 83  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Kringle domain  
Consensus Sequence

<400> 86  
Arg Asp Cys Tyr Ala Gly Asn Gly Glu Ser Tyr Arg Gly Thr Ala Ser  
1 5 10 15

Thr Thr Lys Ser Gly Lys Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro  
20 25 30

His Leu His Arg Phe Thr Pro Glu Arg Phe Pro Glu Leu Gly Leu Glu  
35 40 45

His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ser Glu Gly Pro Trp Cys  
50 55 60

Tyr Thr Thr Asp Pro Asn Val Arg Trp Glu Tyr Cys Asp Ile Pro Gln  
65 70 75 80

Cys Glu Ser

<210> 87

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like  
serine protease Consensus Sequence

<400> 87

Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln  
1 5 10 15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu  
20 25 30

Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser  
35 40 45

Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser  
50 55 60

Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro  
65 70 75 80

Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu  
85 90 95

Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro  
100 105 110

Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly  
115 120 125

Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln  
130 135 140

Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr  
145 150 155 160

Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu  
165 170 175

Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val  
180 185 190

Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser  
 195 200 205

Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser  
 210 215 220

Ser Tyr Leu Asp Trp Ile  
 225 230

<210> 88  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Trypsin  
 Consensus Sequence

<400> 88  
 Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val  
 1 5 10 15

Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser  
 20 25 30

Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser  
 35 40 45

Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr  
 50 55 60

Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn  
 65 70 75 80

Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr  
 85 90 95

Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp  
 100 105 110

Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys  
 115 120 125

Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val  
 130 135 140

Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr  
 145 150 155 160

Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp  
 165 170 175

Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val  
 180 185 190

Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr

195	200	205
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Arg Val Ser Arg Tyr Leu Asp Trp Ile  
210 215

<210> 89  
<211> 79  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Divergent  
subfamily of APPLE domains Consensus Sequence

<400> 89  
Lys Ser Asp Asp Cys Phe Val Arg Leu Pro Asn Thr Lys Leu Pro Asp  
1 5 10 15  
Phe Ser Pro Ile Val Ile Ser Val Ala Ser Leu Glu Glu Cys Ala Gln  
20 25 30  
Lys Cys Leu Asn Ser Asn Cys Ser Cys Arg Ser Phe Thr Tyr Asn Asn  
35 40 45  
Asp Thr Lys Gly Cys Leu Leu Trp Ser Glu Ser Ser Leu Gly Asp Ala  
50 55 60  
Arg Gln Leu Leu Pro Ser Gly Gly Val Asp Tyr Tyr Glu Lys Ile  
65 70 75

<210> 90  
<211> 145  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Lipocalin/cytosolic fatty-acid binding protein  
family Consensus Sequence

<400> 90  
Lys Phe Ala Gly Lys Trp Tyr Leu Val Ala Ser Ala Asn Phe Asp Pro  
1 5 10 15  
Glu Leu Lys Glu Glu Leu Gly Val Leu Glu Ala Thr Arg Lys Glu Ile  
20 25 30  
Thr Pro Leu Lys Glu Gly Asn Leu Glu Ile Val Phe Asp Gly Asp Lys  
35 40 45  
Asn Gly Ile Cys Glu Glu Thr Phe Gly Lys Leu Glu Lys Thr Lys Lys  
50 55 60  
Leu Gly Val Glu Phe Asp Tyr Tyr Thr Gly Asp Asn Arg Phe Val Val  
65 70 75 80

Leu Asp Thr Asp Tyr Asp Asn Tyr Leu Leu Val Cys Val Gln Lys Gly  
85 90 95

Asp Gly Asn Glu Thr Ser Arg Thr Ala Glu Leu Tyr Gly Arg Thr Pro  
100 105 110

Glu Leu Ser Pro Glu Ala Leu Glu Leu Phe Glu Thr Ala Thr Lys Glu  
115 120 125

Leu Gly Ile Pro Glu Asp Asn Val Val Cys Thr Arg Gln Thr Glu Arg  
130 135 140

Cys  
145

<210> 91

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Connexin  
Consensus Sequence

<400> 91

Met Asp Trp Ser Phe Leu Gly Arg Leu Leu Glu Gly Val Asn Lys His  
1 5 10 15

Ser Thr Ala Ile Gly Lys Ile Trp Leu Ser Val Leu Phe Ile Phe Arg  
20 25 30

Ile Leu Val Leu Gly Val Ala Ala Glu Ser Val Trp Gly Asp Glu Gln  
35 40 45

Ser Asp Phe Val Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val Cys  
50 55 60

Tyr Asp Gln Phe Phe Pro Ile Ser His Val Arg Leu Trp Val Leu Gln  
65 70 75 80

Leu Ile Phe Val Ser Thr Pro Ser Leu Leu Tyr Leu Gly His Val Ala  
85 90 95

Tyr Arg Val Arg Arg Glu Glu Lys Leu Arg Glu Lys Glu Glu Glu His  
100 105 110

Ser Lys Gly Leu Tyr Ser Glu Glu Ala Lys Lys Arg Cys Gly Ser Glu  
115 120 125

Asp Gly Lys Val Arg Ile Arg Gly Gly Leu Trp Trp Thr Tyr Val Phe  
130 135 140

Ser Ile Ile Phe Lys Ser Ile Phe Glu Val Gly Phe Leu Tyr Gly Gln  
145 150 155 160

Tyr Leu Leu Tyr Gly Phe Thr Met Ser Pro Leu Val Val Cys Ser Arg  
 165 170 175  
 Ala Pro Cys Pro His Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu  
 180 185 190  
 Lys Thr Ile Phe Ile Val Phe Met Leu Val Val Ser Ala Ile Cys Leu  
 195 200 205  
 Leu Leu Asn Leu Ala Glu Leu Phe Tyr Leu  
 210 215

<210> 92  
 <211> 59  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Src homology 3  
 domains Consensus Sequence

<400> 92  
 Glu Gly Pro Gln Val Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asp Pro  
 1 5 10 15  
 Asp Glu Leu Ser Phe Lys Lys Gly Asp Ile Ile Thr Val Leu Glu Lys  
 20 25 30  
 Ser Asp Asp Gly Trp Trp Lys Gly Arg Leu Gly Thr Gly Lys Glu Gly  
 35 40 45  
 Leu Phe Pro Ser Asn Tyr Val Glu Glu Ile Asp  
 50 55

<210> 93  
 <211> 57  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: SH3 domain  
 Consensus Sequence

<400> 93  
 Pro Lys Val Val Ala Leu Tyr Asp Tyr Gln Ala Arg Glu Ser Asp Glu  
 1 5 10 15  
 Leu Ser Phe Lys Lys Gly Asp Ile Ile Ile Val Leu Glu Lys Ser Asp  
 20 25 30  
 Asp Gly Gly Trp Trp Lys Gly Arg Leu Lys Gly Thr Lys Glu Gly Leu  
 35 40 45  
 Ile Pro Ser Asn Tyr Val Glu Pro Val  
 50 55



<210> 94  
 <211> 91  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fes/CIP4  
 homology domain Consensus Sequence

<400> 94  
 Met Gly Phe Trp Ser Glu Leu Asp Asp Gly Phe Glu Ala Leu Leu Ser  
           1                          5                          10                          15  
 Arg Leu Lys Asn Gly Leu Arg Leu Leu Glu Asp Leu Lys Lys Phe Met  
                           20                          25                          30  
 Arg Glu Arg Ala Lys Ile Glu Glu Glu Tyr Ala Lys Lys Leu Gln Lys  
                           35                          40                          45  
 Leu Ser Lys Lys Leu Arg Ala Val Arg Asp Thr Glu Ser Glu Leu Gly  
           50                          55                          60  
 Ser Leu Arg Lys Ala Trp Glu Val Leu Leu Ser Glu Thr Asp Ala Leu  
           65                          70                          75                          80  
 Ala Lys Gln His Leu Gln Leu Ser Glu Asp Leu  
                           85                          90

<210> 95  
 <211> 94  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fes/CIP4  
 homology domain Consensus Sequence

<400> 95  
 Met Gly Phe Gly Ser Glu Leu Cys Pro Glu Gly His Lys Ala Leu Leu  
           1                          5                          10                          15  
 Ser Arg Gln Asp Asn Glu Leu Arg Leu Leu Glu Glu Met Lys Lys Phe  
                           20                          25                          30  
 Met Ala Glu Arg Ala Lys Ile Glu Lys Glu Tyr Ala Gly Lys Leu Gln  
                           35                          40                          45  
 His Leu Ser Ala Gln Val Gly Lys Gly Pro Ala Thr Ala Glu Gly Glu  
           50                          55                          60  
 Asp Glu Leu Ser Ser Leu Lys Ser Trp Ala Val Ile Leu Ser Glu Thr  
           65                          70                          75                          80  
 Glu Gln Gln Ser Lys Ile His Leu Gln Ile Ser Glu Asp Leu

<210> 96  
 <211> 230  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Trypsin-like  
 serine protease Consensus Sequence

<400> 96  
 Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln  
   1                  5                  10                  15  
 Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu  
                   20                  25                  30  
 Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser  
           35                  40                  45  
 Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser  
       50                  55                  60  
 Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro  
   65                  70                  75                  80  
 Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu  
                   85                  90                  95  
 Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro  
                   100                  105                  110  
 Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly  
           115                  120                  125  
 Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln  
   130                  135                  140  
 Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr  
  145                  150                  155                  160  
 Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu  
                   165                  170                  175  
 Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val  
                   180                  185                  190  
 Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser  
           195                  200                  205  
 Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser  
   210                  215                  220  
 Ser Tyr Leu Asp Trp Ile  
  225                  230

<210> 97  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Trypsin  
 Consensus Sequence

<400> 97  
 Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val  
   1                  5                  10                  15  
 Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser  
                   20                  25                  30  
 Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser  
                   35                  40                  45  
 Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr  
                   50                  55                  60  
 Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn  
   65                  70                  75                  80  
 Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr  
                   85                  90                  95  
 Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp  
                   100                  105                  110  
 Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys  
                   115                  120                  125  
 Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val  
   130                  135                  140  
 Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr  
  145                  150                  155                  160  
 Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp  
                   165                  170                  175  
 Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val  
                   180                  185                  190  
 Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr  
                   195                  200                  205  
 Arg Val Ser Arg Tyr Leu Asp Trp Ile  
   210                  215

<210> 98  
 <211> 24

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: NOV5 Primer 1  
  
 <400> 98  
 ctcccactcc tgctgcttct gact 24  
  
 <210> 99  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: NOV5 Primer 2  
  
 <400> 99  
 aaggctgggc ctaaccagc ctcac 25  
  
 <210> 100  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: NOV7 Primer 1  
  
 <400> 100  
 catgaactgg gcatttctgc agg 23  
  
 <210> 101  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: NOV7 Primer 2  
  
 <400> 101  
 ttatctgctg atctcgcagg ttatgga 27  
  
 <210> 102  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: NOV8 Primer 1  
  
 <400> 102  
 ctgacaggcc ctggtgtgtg at 22

<210> 103  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV8 Primer 2

<400> 103  
tcacacatgt ttcattgtggg agttaga

27

<210> 104  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV9 Primer 1

<400> 104  
gagtggagagg tcggacagac tgtg

24

<210> 105  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV9 Primer 2

<400> 105  
actcatgcaa cttgcttctc tcactct

27

<210> 106  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV10b Primer  
1

<400> 106  
cctatgagcc tgatgctgga tgac

24

<210> 107  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV10b Primer

2

<400> 107  
aggactcaga ggagggagtc ctgag 25

<210> 108  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag4164 Forward

<400> 108  
gcactacaag tggaagcctt ac 22

<210> 109  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag4164 Probe

<400> 109  
ctcaagtaga agccgactta tgcaaa 26

<210> 110  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag4164 Reverse

<400> 110  
tcaaadcctt ctgcgataca gt 22

<210> 111  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1313b  
Forward

<400> 111  
cagctgcacg attaataag at 22

<210> 112  
<211> 25

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag1313b Probe  
  
 <400> 112  
 aggtcttgga ctggccttca ccatt 25  
  
 <210> 113  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag1313b  
 Reverse  
  
 <400> 113  
 ccaaagttgt gtccagactc at 22  
  
 <210> 114  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag2197 Forward  
  
 <400> 114  
 ccaaggaaga cctcttcatc tt 22  
  
 <210> 115  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag2197 Probe  
  
 <400> 115  
 tcttgcttac ggcataagcg ctctct 26  
  
 <210> 116  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag2197 Reverse  
  
 <400> 116  
 ttcatttcta tgggacctca ga 22

<210> 117  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag708 Forward  
  
 <400> 117  
 aaagatggga ctcgtcatga c 21  
  
 <210> 118  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag708 Probe  
  
 <400> 118  
 cacgccatct tactgactgg tctgga 26  
  
 <210> 119  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag708 Reverse  
  
 <400> 119  
 gtgcaaattcc caaagtgtca 20  
  
 <210> 120  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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 <400> 120  
 gcactacaag tggaagcctt ac 22  
  
 <210> 121  
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<400> 121  
 ctcaagtaga agccgactta tgcaaa 26

<210> 122  
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<220>  
 <223> Description of Artificial Sequence: Ag4164 Reverse

<400> 122  
 tcaaatcctt ctgcgatata gt 22

<210> 123  
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<220>  
 <223> Description of Artificial Sequence: Ag2197 Forward

<400> 123  
 ccaaggaaga cctcttcatc tt 22

<210> 124  
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 tcttgcttac ggcataagcg ctctct 26

<210> 125  
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 <223> Description of Artificial Sequence: Ag2197 Reverse

<400> 125  
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<210> 126  
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 aaagatggga ctcgtcatga c 21  
  
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 Forward  
  
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 cagctgcacg attaatgaag at 22  
  
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 Reverse  
  
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 ccaaagttgt gtccagactc at 22  
  
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<400> 135 tttcaagaca ccctgtgata cc	22
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<400> 137 cagaggaatg aaggcataga tg	22
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<400> 138 gtaggcaaag ggactcactg t	21
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 <210> 142  
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 <220>  
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 <400> 148  
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 <210> 149  
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 <212> DNA  
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 <223> Description of Artificial Sequence: Ag3797 Reverse  
  
 <400> 149  
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<210> 150  
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<220>  
<223> Description of Artificial Sequence: Ag2439 Forward

<400> 150  
tatcatcact tgtgatggca aa 22

<210> 151  
<211> 26  
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<220>  
<223> Description of Artificial Sequence: Ag2439 Probe

<400> 151  
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<210> 152  
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<220>  
<223> Description of Artificial Sequence: Ag2439 Reverse

<400> 152  
aaacttctct cccagggtac aa 22

<210> 153  
<211> 22  
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<220>  
<223> Description of Artificial Sequence: Ag2771 Forward

<400> 153  
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<210> 154  
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<220>  
<223> Description of Artificial Sequence: Ag2771 Probe

<400> 154 tctgggtaag aagtactgcc ccaaacg	27
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<400> 155 ggctcttcat ctttgatga a	21
<210> 156 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Ag1674 Forward	
<400> 156 ctcactcacc acaagggagt aa	22
<210> 157 <211> 27 <212> DNA <213> Artificial Sequence	
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<400> 157 tgacatcaaa ctcaacagtt cccagga	27
<210> 158 <211> 22 <212> DNA <213> Artificial Sequence	
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<400> 158 gtctaggaga gagctgagca aa	22
<210> 159 <211> 78 <212> PRT <213> Artificial Sequence	



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<223> Description of Artificial Sequence: PAN domain  
Consensus Sequence

<400> 159

Cys Ser Ser Phe Val Arg Val Pro Gly Arg Ser Leu Ser Gly Asn Asp  
1 5 10 15

Ile Ser Val Val Asn Val Pro Ser Leu Glu Glu Cys Ala Ala Leu Cys  
20 25 30

Leu Glu Glu Pro Arg Val Cys Arg Ser Phe Thr Tyr Asn Asn Lys Ser  
35 40 45

Lys Gln Cys Leu Leu Lys Ser Glu Ser Ser Gly Ser Leu Pro Arg Leu  
50 55 60

Lys Arg Pro Ser Gln Lys Val Asp Tyr Tyr Glu Lys Ser Cys  
65 70 75

<210> 160

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Connexin  
homologues Consensus Sequence

<400> 160

Ser Val Trp Gly Asp Glu Gln Ser Asp Phe Thr Cys Asn Thr Gln Gln  
1 5 10 15

Pro Gly Cys Glu Asn Val Cys Tyr Asp Gln Phe Phe Pro Ile Ser His  
20 25 30

Val Arg